ADL33627.1
CP001810.1:1076129-1092190
Butyrivibrio proteoclasticus B316

LRRs Transglutaminase ? ? Peripla_BP_4 ? ? ? PBECR4 Acetyltransf_7 ? SATase_N Hexapep Dus ETRAMP Flg_bb_rod LlgE_F_G_D1 Flg_bbr_C Ninein_long_CC

AOZ94846.1
CP017771.1:2914-17327
Paenibacillus crassostreae

HxlR ADH_N ADH_zinc_N GFA PedC-like ? DndB ? PBECR4 ? Phage_int_SAM_1 Phage_integrase ? ? MerR_1 Ninein_long_CC ? Pro_dh

AOZ94867.1
CP017772.1:150-20568
Paenibacillus crassostreae

Ninein_long_CC ? Esterase ? ? DndB DndB ? ? ? PBECR4 Phage_int_SAM_1 Phage_integrase HTH_36

APZ50253.1
CP019433.1:978815-996019

Jeotgalibaca sp. PTS2502

? ? ? ? ? TMP_3 ? PBECR4 S4 Ribosomal_S4 EzrA Aminotran_5 ThiI_fer THUMP ThiI AhpC-TSA tRNA-synt_1 Anticodon_1 Val_tRNA-synt_C Mur_ligase_M Mur_ligase_C

AWK50556.1
CP029329.1:1300754-1320091
Clostridium beijerinckii

? TnpB_IS66 LZ_Tnp_IS66 zf-IS66 DDE_Tnp_IS66 DDE_Tnp_IS66_C Tn7_TnsA-like_N Tn7_Tnp_TnsA_C TnsB_N HTH_TnsB Mu-transpos_C AAA_22 TniQ TnsD PBECR4 dCache_1 HAMP MCPsignal MCPsignal Phosphorylase HTH_18 Rubrerythrin RUBY_RBDX ? HutD 5-FTHF_cyc-lig

CAD5901733.1
CAJGUR010000057.1:51670-66204
Carnobacterium maltaromaticum

His-Kinase His-Kinase HAMP Trans_reg_C Receiver ? ABC_tran FtsX ? DUF2196 DUF1456 DUF1456 PBECR4 Hydrolase_3 APH AlkZ-like Adenine_glyco AMP-binding DUF1846 DUF1846_C Peptidase_S9

CAH0534888.1
CAKASQ030000004.1:283-11817
Oscillospiraceae bacterium

ATLF SLH NLPC_P60 ? ? ? ? PBECR4 DNA_methylase DNA_methylase HerA-FtsK PrgI ? ParE_toxin PhdYeFM_antitox TrbL_2

CAH0535565.1
CAKASQ030000008.1:7038-17109
Oscillospiraceae bacterium

? ? DUF6291 HicB ? ParE_toxin ? PBECR4 ? NTP_transf_2 HEPN ABC_tran ABC_membrane ABC_tran RsgA_GTPase ABC_membrane ? HTH_18

CAK1222097.1
CAUZLH010000001.1:164676-175867
Fructobacillus evanidus

DUF1617 BppU_N Phage_YomQ_N Phage_XkdX PUB2_N Phage_holin_6_1 Amidase_5 ZoocinA_TRD PBECR4 UPRTase Peptidase_S11 ? Peptidase_M24 Methyltr_RsmF_N Methyltr_RsmB-F RsmF_methylt_CI Methyltranf_PUA DUF1831 His_Phos_1

CAK1235005.1
CAUZLN010000003.1:41032-60283
Fructobacillus fructosus

EF_TS AA_kinase RRF Choline_bind_3 Amidase_5 DUF2130 tRNA-synt_2e tRNA_synt_2f DALR_1 PBECR4 GmrSD_N GmrSD_C Peptidase_S9 Tricorn_N GTP_EFTU GTP_EFTU_D2 RF3_C EFG_C LepA_C ADH_N ADH_zinc_N_2 PrmA PUA_4 Methyltrans_RNA ?

CAK1249590.1
CAUZLR010000009.1:5724-20258
Fructobacillus fructosus

DltX ? DUF915 TPM_phosphatase LemA Mem_trans 2-Hacid_dh_C PBECR4 DUF4811 MFS_1 TetR_N TetR_C_8 LysR_substrate HTH_1 AA_permease_2 BPD_transp_1 ABC_tran

CDB87356.1
FR887078.1:298-6901
Firmicutes bacterium CAG:170

DUF1540 2-Hacid_dh_C ? ? Cluap1 HTH_26 Fic PBECR4 ?

CUO12971.1
CYYL01000016.1:33251-45179
Faecalibacterium prausnitzii

NUDIX RicinB_lectin_2 RicinB_lectin_2 ? ? Acetylase Trp_repressor DJ-1_PfpI PBECR4 FAA_hydrolase TatA_B_E CRLF3_N TatA_B_E TatC ROK ABC_tran ABC_membrane Ala_racemase_N

DAF00658.1
BK055943.1:29617-36241
Caudoviricetes sp.

? ? ? CBM_5_12 NLPC_P60 SH3_3 Phage_holin_Dp1 ? PBECR4 Phage_integrase Phage_int_SAM_1 ? ? ? ? DUF6290 ?

DAH77474.1
BK024147.1:8458-16277
Bacteriophage sp.

? ? ? PhageMin_Tail ? ? ? PBECR4 ? ? ? DUF6575 ? zf-C2HC5 ?

DAJ37187.1
BK038871.1:32015-34997
Caudoviricetes sp.

? ? ? ? ? ? ? PBECR4 ? ? ? ? ?

DAJ54250.1
BK043505.1:1-3482
Caudoviricetes sp.

? ? ? ? ? ? ? PBECR4 ? ?

DAJ54410.1
BK043509.1:1-10353
Bacteriophage sp.

Phage_fiber_rpt Phage_fiber_rpt ? Phage_head_fibr Peptidase_G2 Peptidase_M23 ? Phage_holin_6_1 FlaC_arch PBECR4 ? HTH_3 Cas_Csd1 ? HTH_3 Rep3_N

DAK72223.1
BK047663.1:3697-11985
Caudoviricetes sp.

Collagen LRRs ? Amidase_2 LysM PG_binding_1 DUF722 ? ? PBECR4 ? ? ? Phage_integrase TraX-like HTH_3 ? ?

DAM38777.1
BK051841.1:3883-10614
Caudoviricetes sp.

? Mu_Gam-Sipho_Gp157-TOTE ? ? RepB-RCR_reg RepB-RCR_reg ? PBECR4 ? Sigma70_r4 Sigma70_r2 ? ? ? HmpF ?

DAO23223.1
BK049155.1:7803-14689
Caudoviricetes sp.

? Glyco_hydro_25 ? ? Phage_integrase Phage_int_SAM_3 Arm-DNA-bind_4 ? ? PBECR4 MarR Phage_min_cap2 Peptidase_S24 HTH_3 ? ? ORF6N HTH_3 ?

DAR20191.1
BK056956.1:1-17619
Caudoviricetes sp.

SOG2 ? ? ? PBECR4 ? bZIP_1 DUF6558 DUF6558_C ? ? ? DUF6273

DAX73955.1
BK040120.1:26508-34040
Caudoviricetes sp.

Prophage_tail SHE3 DUF859 JAKMIP_CC3 Phage_holin_4_1 Phage_holin_1 ? ? PBECR4 Amidase_2 Choline_bind_1 Choline_bind_3 Choline_bind_1 ? ?

DAZ42629.1
BK026827.1:45001-55455
Caudoviricetes sp.

Zn_ribbon_4 ? ? Zn_ribbon_IS1595 DUF8255 CENP-F_leu_zip ? ? PBECR4 ? ? Big ? ? ? ?

EAD5986708.1
AAAOBF010000001.1:193-8869
Listeria monocytogenes

Sipho_tail SPP1_Dit Prophage_tail Phage_RBD_prop DUF2510 ? DUF16 Phage_holin_1 Peptidase_M15_4 DUF3597 DUF5776 PBECR4 AP2

EDP23067.1
DS483488.1:7071-18806
Faecalibacterium prausnitzii M21/2

MerR_1 Relaxase NikA-like ? ? ? B12-binding_2 Lipoprotein_Ltp Lipoprotein_Ltp PBECR4 GIY-YIG ? AAA_15 DUF6061 oligo_HPY ABC_tran oligo_HPY ABC_tran BPD_transp_1 OppC_N

EGO9014299.1
AAXEOO010000065.1:1-1323
Enterococcus faecalis

AAA_2 PBECR4

EME3574602.1
ABPXRJ010000037.1:18936-23772
Enterococcus faecium

? ? ? ? Endonuclea_NS_2 ? ? PBECR4

EOS26495.1
KE159582.1:431694-444589
Lachnospiraceae bacterium 3-1

? ? Phage_pRha MTES_1575 ? ? ? ? PBECR4 Peptidase_M1_N ? DnaJ ? HTH_26 DUF7674 ?

EOS74606.1
KE159720.1:84925-103390
Dorea sp. 5-2

YscJ_FliF_C YscJ_FliF FliE Flg_bb_rod SLT 4HB_MCP_1 HAMP MCPsignal MCPsignal Malic_M malic malic Beta-lactamase PBECR4 Radical_SAM Radical_SAM BATS MMR_HSR1 MMR_HSR1_Xtn HydF_dimer HydF_tetramer DUF4143 AAA_14 FGGY_C FGGY_N Fucose_iso_C Alpha-L-AF_C ASD1_dom

GFI03610.1
BLLW01000048.1:434-10171
Lachnospiraceae bacterium

PBECR4 Rce1-like HAD_2 S1 S1 S1 CHIM_prot RUBY_RBDX Flavin_Reduct ABC_tran ABC_tran_Xtn ABC_tran Phosphorylase

GFI24373.1
BLMC01000170.1:241-5242
Lachnospiraceae bacterium

? PBECR4 Relaxase_C Relaxase Toprim_2 DUF3991 TnpW ?

GFI31243.1
BLME01000470.1:482-1126
Lachnospiraceae bacterium

PBECR4

GHU52754.1
BNUF01000030.1:6883-21675
Clostridia bacterium

P-loop_TraG Peptidase_M23 NLPC_P60 ? CD1107-like HTH_3 Toprim Topoisom_bac PAPS_reduct PAPS_reduct PBECR4 ? Acetyltransf_7 Macro HTH_3 PhdYeFM_antitox

GHU57806.1
BNUF01000180.1:1541-3971
Clostridia bacterium

RNase_H ? PBECR4

HAD77029.1
DLZS01000057.1:2748-17590
Dialister sp.

? ? AAA AAA_lid_3 ? ? ? Sel1 Sel1 Sel1 Sel1 PBECR4 ? DUF445 DUF445 Ala_racemase_N Ala_racemase_C Phage_integrase Phage_int_SAM_3 ? EC042_2821 DUF3644

HAP4873295.1
DACBJM010000018.1:21075-35152
Enterococcus faecalis

Sipho_tail Prophage_tail_N2 Prophage_tail ? ? Spectrin_Anc-1_2 Phage_holin_1 ? PBECR4 pEK499_p136 QueT FemAB ECF_trnsprt Flavoprotein DFP DFP ?

HBB13666.1
DNLM01000128.1:1-7178
Treponema sp.

? ? PBECR4 TEN_YD-shell TEN_YD-shell ? ? ? ?

HBI61650.1
DNTZ01000341.1:1-7553
Lachnospiraceae bacterium

Glyco_hydro_59 Voltage_CLC FUR RUBY_RBDX Rubrerythrin Rubrerythrin Aminotran_1_2 Hydrolase_3 PBECR4 ? Phage_integrase

HBY20664.1
DOSN01000154.1:1-6845
Clostridiales bacterium

PBECR4 HIRAN ? ? ? Oxidored_q6 Fer4_9 DUF8371 AAA-ATPase_like

HBY72190.1
DORJ01000226.1:46-6470
Lachnospiraceae bacterium

PBECR4 Acetylase ? Epimerase Hydrolase_3 AsnA Methyltransf_11

HDV6059853.1
DAPIGF010000035.1:16321-24522
Staphylococcus pseudintermedius

TT1_Tal Prophage_tail_N2 Prophage_tail ? Lipase_GDSL_2 BppU_N EMC7_beta-sandw Phage_holin_4_1 Amidase_2 SH3b_P2 PBECR4

HDZ6482743.1
DAPWYT010000114.1:280-692
Staphylococcus aureus

PBECR4

HEL1728893.1
DARZBR010000035.1:72-1199
Streptococcus suis

PBECR4 Paratox

HEL1991109.1
DARZGN010000003.1:60386-86767
Streptococcus suis

P-loop_TraG Peptidase_M23 Phage_lysozyme2 CHAP ? TPR_MLP1_2 Gram_pos_anchor Adhesin_P1_N GbpC AgI_II_C2 AgI_II_C2 Antigen_C MucBP MucBP MucBP SSSPR-51 Gram_pos_anchor PBECR4 ? Methyltransf_25 Eco57I WH_1 DUF8437 Helicase_dom Helicase_C DUF5962 DnaJ ? Zn_ribbon_DnaG DUF3991 Toprim_2 DUF5965

HEM3718372.1
DASEXU010000079.1:381-5035
Streptococcus suis

DUF4238 MmeI_C MmeI_TRD MmeI_Mtase MmeI_hel MmeI_N PBECR4

HEM5173945.1
DASFYU010000041.1:279-11487
Streptococcus suis

PBECR4 SSB DUF7413 Helicase_C Helicase_dom DUF8437 WH_1 Eco57I ? ? DUF3990 CD1107-like CD1107-like ?

HIT08536.1
DVKD01000027.1:154788-165172
Candidatus Merdivicinus faecavium

HD ABC_tran ABC_membrane DHDPS SIS SIS ? Mn_catalase ? PBECR4 Choline_bind_3 Choline_bind_3 Choline_bind_3 Peptidase_M23 ? ? CBM_5_12

HIU58112.1
DVNB01000100.1:15220-25276

Candidatus Ornithomonoglobus merdipullorum

TPP_enzyme_C PFOR_II POR_N Fer4_7 AMP-binding AMP-binding_C OmdA DUF4368 TPRs PBECR4 ? RepA_N DUF3847 MobA_MobL HTH_18

HIX24970.1
DXFM01000030.1:10403-27215
Candidatus Lachnoclostridium avicola

TSCPD Ribonuc_red_lgC MerR_1 LysR_substrate HTH_1 IMS_C IMS DUF362 Fer4_8 Aldo_ket_red Calcineurin PBECR4 GARS_C GARS_A GARS_N Formyl_trans_N AIRS_C AIRS AIRC Peptidase_M29 DUF6142 VanZ

HJC48338.1
DWWL01000063.1:11652-34977
Candidatus Lachnoclostridium pullistercoris

RUBY_RBDX Rubrerythrin ? Rubrerythrin RUBY_RBDX FGGY_C FGGY_N Cation_ATPase_C Hydrolase_3 Cation_ATPase E1-E2_ATPase Cation_ATPase_N LuxS Isoamylase_C PBECR4 ABC_tran_CTD ABC_tran ABC_tran_Xtn ABC_tran Synaptojanin ? LRRs LRRs LRRs DUF3298 ? AP-ATPase

HVI39820.1
DATLIV010000224.1:1-3604
Anaerovoracaceae bacterium

AA_permease PBECR4 AA_permease

KGF53242.1
KN174167.1:127289-142593

Flavonifractor plautii 1_3_50AFAA

DUF5697 ? ? SepF Phage_int_SAM_1 Phage_integrase Sirtuin STALD TIR PBECR4 HTH_3 Trans_reg_C Helicase_C DNA_pol3_beta DNA_pol3_beta_2 ? ? ?

KOP65918.1
LITP01000001.1:2717031-2734126
Bacillus sp. FJAT-18019

DUF418 HisKA_3 His-Kinase Receiver GerE MarR adh_short_C2 Arabinose_bd HTH_18 adh_short PBECR4 Antibiotic_NAT His-Kinase His_kinase Receiver His-Kinase His-Kinase 7TMR-DISM_7TM DUF6932 ? HTH_Mga Mga PNPase ECF_trnsprt

MBC9704720.1
JACUTK010000191.1:549-4018
Enterococcus sp.

HTH_3 HTH_36 PBECR4 ?

MBD5112202.1
JAAVIC010000017.1:664-13950
Oscillospiraceae bacterium

Mob_Pre DUF6017 Metallophos_2 PBECR4 T1-F ? Flavodoxin_5 PAS ? DUF1015 PHP_C PHP DNA_pol_A DNA_polI_exo1 5_3_exonuc 5_3_exonuc_N

MBD5393572.1
JAAVBZ010000008.1:96623-113193
Lachnospiraceae bacterium

RF-1 PCRF SEC-C SecA_SW P-loop_SecA P-loop_SecA SecA_DEAD PALP ? ABC_tran ? ABC2_membrane_6 PBECR4 Beta_elim_lyase MreB_Mbl ? ? AAA-ATPase_like DUF5105 ABC_tran

MBD5424059.1
JAAVAY010000062.1:145-10127
Allobaculum sp.

TPRs ? Glycos_transf_2 SRP54_N SRP54 SRP_SPB PBECR4 Ribosomal_S16 KH_KhpA-B RimM PRC_RimM tRNA_m1G_MT Peptidase_M15_4 Ribosomal_L19

MBD5451963.1
JAAVAF010000066.1:54-14839
Lachnospiraceae bacterium

HMA E1-E2_ATPase Hydrolase DEAD DEAD_2 Helicase_C_2 UPF0175 ? Asp_protease_2 Fic PBECR4 N_methyl A24_N_bact Peptidase_A24 PilM_2 PilM_2 PilO N_methyl ? N_methyl

MBD5631796.1
JAAUYR010000012.1:32307-41033
Clostridia bacterium

HTH_3 ? DUF2726 Zn_ribbon_recom DUF7345 HTH_19 ? Zn_Ribbon_1 PBECR4 Resolvase Recombinase Zn_ribbon_recom HTH_24 Transpeptidase

MBD9054722.1
RKFB01000009.1:41222-57704
Eubacterium ventriosum

Asp_decarbox Pantoate_ligase Pantoate_transf DUF2520 Rossmann-like Trigger_C FKBP_C ADSL_C Lyase_1 Pribosyltran GATase_7 PBECR4 DUF5944 Sigma70_r4_2 Sigma70_r2 GatB_Yqey GatB_N Amidase GatC Lactamase_B_3 SBP_bac_3

MBD9241588.1
RKCM01000132.1:1-7455
Oscillospiraceae bacterium

? Trp_repressor DJ-1_PfpI PBECR4 FAA_hydrolase Peptidase_M24 Creatinase_N TatA_B_E TatA_B_E TatC ROK HTH_3

MBD9365110.1
JACXBX010000005.1:111-10287
Leuconostoc mesenteroides

DUF5906 Capsid_pestivir HTH_3 DUF7702 ? PBECR4 P8 HTH_3 DUF6442 ABC_tran DrrA1-3_C ABC2_membrane_3 ? OpuAC BPD_transp_1

MBE1553178.1
JADBEL010000001.1:227044-238138
Sporosarcina limicola

ParE-like_toxin TetR_C_6 TetR_N DUF2070 Rce1-like PadR Vir_act_alpha_C Rce1-like ? PBECR4 FMN_red DUF3238 TENA_THI-4 HK Phos_pyr_kin TMP-TENI ThiW

MBE5827063.1
SVGA01000019.1:21052-33863
Butyrivibrio sp.

DUF2178 Sigma70_r2 Sigma70_r4_2 ? ? Penicillinase_R Peptidase_M56 HTH_3 PBECR4 PadR HAAS FTSW_RODA_SPOVE HTH_3 ? Sigma70_r2 Sigma70_r4_2 ? ?

MBE5917286.1
SVES01000033.1:6871-24289
Pseudobutyrivibrio ruminis

? ? ? Eco57I ? CRISPR_Cas2 ? PBECR4 DUF723 DUF2726 ? ? ? ? ? Baculo_PP31

MBE5926520.1
SVEP01000011.1:65805-73043
Lachnospiraceae bacterium

PepSY ABC_trans_CmpB PBECR4 LMWPc DUF5714 ? ? DUF874 MFS_1 Peptidase_M23

MBE5928335.1
SVEM01000008.1:2121-15886
Lachnospiraceae bacterium

Peptidase_S8 DUF6376 Zn_dep_PLPC LRRs DUF3021 LytTR ABC2_membrane ABC_tran Nitroreductase GGGtGRT PBECR4 MTPAP-like_central ? ? Nitroreductase YunG Glyco_hydro_43 GH43_C2 Glyco_hydro_43

MBE6093636.1
SVBY01000113.1:582-5690
Selenomonas ruminantium

PBECR4 TPS YDG YDG YDG YDG YDG YDG ?

MBE6100530.1
SVBX01000001.1:45570-65288
Selenomonas ruminantium

HTH_29 HTH_33 PriA_3primeBD DEAD Zn_ribbon_PriA Helicase_C PriA_C GatC Amidase GatB_N GatB_Yqey HAD_2 TRAM tRNA_U5-meth_tr PBECR4 ? Methyltransf_25 RUBY_RBDX Flavin_Reduct SDF DUF362 DUF4127 Cons_hypoth95

MBE6102167.1
SVBX01000015.1:18462-36988
Selenomonas ruminantium

Peripla_BP_2 FecCD ABC_tran HD AAA_14 DUF4143 Fic HsdM_N N6_Mtase Methylase_S Methylase_S PBECR4 REase SWI2_SNF2 T1R_D3-like AAA_18 PfkB FecCD ABC_tran Peripla_BP_2 PAS_10 Hemerythrin

MBE6964576.1
SVLF01000002.1:87628-97067
Oscillospiraceae bacterium

YomN ? ? YonV_C ? Stc1 RNA_pol_A_CTD PBECR4 HTH_26 Sipho_Gp157 DnaJ ? ? ? ?

MBE6991648.1
SVKU01000005.1:639-11130
Oscillospiraceae bacterium

Metalloenzyme C_GCAxxG_C_C RecG_dom3_C Helicase_C DEAD RecG_wedge Malic_M malic Ribosomal_S20p Peptidase_A25 Peptidase_A25 SBP_bac_1 PBECR4 DUF6809

MBE7032817.1
SVJW01000003.1:58921-78923
Oscillospiraceae bacterium

SBP_bac_1 Glyco_hydro_42M GHL6 AraC_binding HTH_18 ASRT Peptidase_M24 Creatinase_N MlrC_C DUF1485 Peripla_BP_1 LacI PBECR4 ? Phage_integrase Phage_int_SAM_3 ? Pox_D5 DUF5906 D5_N ? GATase_6 Amidoligase_2 LIM

MBE7727869.1
SVDP01000120.1:310-11130
Enterocloster citroniae

Rrf2 ABC_tran Pyr_redox_2 HTH_3 HTH_36 Toprim_2 DUF3991 Sel1 Sel1 Sel1 Sel1 Sel1 Sel1 Sel1 Sel1 Sel1 MobL PBECR4 ? ?

MBF0579031.1
JADGIS010000032.1:1-11027
Erysipelotrichaceae bacterium RD49

? TPRs ? Glycos_transf_2 ? SRP54_N SRP54 SRP_SPB PBECR4 Ribosomal_S16 KH_KhpA-B RimM PRC_RimM tRNA_m1G_MT Peptidase_M15_4 Ribosomal_L19 Peptidase_S26

MBG9791000.1
LDII01000095.1:50750-60923
Brevibacillus laterosporus

? ? MecA Bro-N ANT ? ? AbiTii PBECR4 DNA_ligase_A_M DUF3800 ?

MBI9095441.1
JAEINL010000042.1:15150-30636
Sphaerochaeta sp.

? NAD_Gly3P_dh_C NAD_Gly3P_dh_N Acetyltransf_10 ? Pyr_redox_2 Rubredoxin_C Glyco_hydro_36C Melibiase Glyco_hydro_36N ? PBECR4 REase-ARP TonB_C ExbD ExbD MotA_ExbB TonB_dep_Rec_b-barrel Plug ?

MBK5200323.1
JAENWY010000023.1:260-16219
Spirochaetaceae bacterium

NikA-like DrHyd SocA_Panacea MqsA_antitoxin ? ? HTH_36 ? ? Phage_integrase ? ? Rep3_N Rep3_C ? ?

MBK5201902.1
JAENWY010000296.1:233-2509
Spirochaetaceae bacterium

? HTH_36 PBECR4

MBN2849347.1
JAFGUV010000097.1:1-6573
Erysipelotrichaceae bacterium

PP_kinase_C PP_kinase_C_1 PP_kinase PP_kinase_N Ppx-GppA PBECR4 DUF2620 YhfT HTH_41 YhfZ_C

MBO4288617.1
JAGAEH010000023.1:1-2904
Lachnospiraceae bacterium

RNase_T PBECR4 Peptidase_M48_N Peptidase_M48

MBO4322683.1
JAGADR010000206.1:1-5645
Clostridia bacterium

Amidase_3 RecG_dom3_C Helicase_C DEAD RecG_wedge PBECR4 Esterase GalP_UDP_transf GalP_UDP_tr_C

MBO4639376.1
JAFZWX010000117.1:15-11309
Treponema sp.

? ? PBECR4 Poly_A_pol_cat Acyltransferase DAGK_cat YegS_C Hydrolase PUA_3 Methyltrans_SAM IPT IPPT TP_0927

MBO4639662.1
JAFZWX010000137.1:1-12568
Treponema sp.

? ABC_tran BioY AMP-binding AMP-binding_C_2 ACT_8 LRRs LRRs LRRs LRRs LRRs LRRs LRRs Flg_new Flg_new Flg_new Flg_new PBECR4 HNH GmrSD_N EcoRI_methylase

MBO5097616.1
JAGAQT010000087.1:1-14553
Agathobacter sp.

Big-like Big Alpha-amylase Alpha-amylase_C PBECR4 IMP_cyclohyd AICARFT_IMPCHas PhdYeFM_antitox ParE_toxin Mem_trans ADDB_N UvrD_C PDDEXK_1 UvrD-helicase UvrD_C PDDEXK_1

MBO5099576.1
JAGARF010000236.1:30-5322
Clostridia bacterium

NifU_N GGGtGRT PBECR4 DUF7204 GTP_EFTU EF-G_D2 EFG_III EFG_IV EFG_C

MBO5127087.1
JAGARE010000393.1:183-2310
Clostridia bacterium

Fer4_20 Pyr_redox_2 PBECR4

MBO5207845.1
JAGAPK010000006.1:3013-25119
Lachnospiraceae bacterium

ABC_tran FtsX MacB_PCD FtsX SpoIID Virul_fac_BrkB Phe_tRNA-synt_N tRNA-synt_2d tRNA_bind B3_4 B5 tRNA_synthFbeta FDX-ACB Peptidase_M18 PBECR4 Queuosine_synth PilZ VanZ EPSP_synthase ACT PDH_C PDH_N GTP_EFTU EF-G_D2 EFG_III EFG_IV EFG_C tRNA-synt_1 tRNA-synt_1_2 tRNA-synt_1 Anticodon_1

MBO5237903.1
JAGAOO010000030.1:12644-28958
Lachnospiraceae bacterium

? ? ? SpaA SpaA SpaA UPF0175 ? AAA_14 DUF4143 PBECR4 HTH_5 HMA E1-E2_ATPase Hydrolase HD Mn_catalase Zn_ribbon_recom Recombinase Resolvase ?

MBO5238425.1
JAGAOO010000045.1:1-9145
Lachnospiraceae bacterium

ABC2_membrane_3 ? HTH_3 Uncharacterised_IM_YidI ? HD_5 ? PBECR4 DUF2971 ?

MBO5372095.1
JAGALK010000048.1:759-7578
Lachnospiraceae bacterium

Ig_Eae Voltage_CLC AraC_binding HTH_18 DegV PBECR4 Sigma70_ECF ? HNH

MBO5416746.1
JAGAKG010000066.1:1-10436
Clostridia bacterium

? ? SSB NrS1-1_pol-like_HBD ? ArdcN MPTase-PolyVal ? PBECR4 ? ? ? ? ? ? ?

MBO5452957.1
JAGAJK010000034.1:293-13129
Clostridia bacterium

Glyco_hydro_39 Amidohydro_2 CRS1_YhbY NifU_N GGGtGRT PBECR4 Polbeta HepT-like HTH_3 tRNA_anti-like DUF4325 His-Kinase HTH_24 DNA_topoisoIV DNA_gyraseB_C Toprim DNA_gyraseB His-Kinase

MBO5570881.1
JAGAGV010000512.1:77-6087
Clostridia bacterium

YgbA_NO ? Flavodoxin_2 SpaA Gram_pos_anchor PBECR4 ? ? PhdYeFM_antitox

MBO5590376.1
JAGAGQ010000053.1:4347-15738
Acidaminococcaceae bacterium

MatE Polysacc_synt RUBY_RBDX Rubrerythrin C_GCAxxG_C_C Glycos_transf_2 DUF2231 PMT_2 RelB AAA_2 ClpB_D2-small PBECR4 ?

MBO6131118.1
JAGBOA010000018.1:276083-292455
Treponema sp.

Rho_N Rho_RNA_bind ATP-synt_ab Ribosomal_L31 Bax1-I ComFB Aconitase_C Aconitase Aconitase FGS FGS PBECR4 FGS FGS HRDC RVT_1 Beta-prop_THOC3 Beta-prop_THOC3 ? ?

MBO6205024.1
JAGBML010000538.1:1-7426
Selenomonas sp.

TP_methylase HEM4 ALAD Aminotran_3 PBECR4 SLFN_AlbA_2 HATPase_c_4 Fic-like_C AbiH

MBP3234329.1
JAGBKD010000095.1:88-5972
Eubacterium sp.

? Receiver ComGE Trans_reg_C His-Kinase His-Kinase ABC_tran FtsX FtsX PBECR4

MBP3280818.1
JAGBIY010000002.1:61708-76762
Treponema sp.

UPF0227 ? Gln-synt_C-ter Gln-synt_C GSIII_N Acyltransferase ? ? ? PBECR4 ? PIN PDDEXK_2 AbiEii ? ? ?

MBP3282536.1
JAGBIY010000034.1:1-7390
Treponema sp.

RBD_DEAH11 SH3_3 SH3_3 LPAM_1 ? DUF6985 NADase_transloc NADase_transloc PBECR4 LPAM_1 TEN_YD-shell ?

MBP3319403.1
JAGBHY010000250.1:280-5622
Ruminiclostridium sp.

? ? PBECR4 ? ? RecG_dom3_C Helicase_C DEAD RecG_wedge

MBP3359904.1
JAGBHE010000029.1:2462-15002
Clostridia bacterium

F_bP_aldolase Lyx_isomer PfkB ParE_toxin ? Acetylase Cu_amine_oxidN1 PBECR4 ADH_Fe_C Fe-ADH CMD Cupin_2 MerR_1 MerR-DNA-bind DEDD_Tnp_IS110 Transposase_20 RelB Radical_SAM

MBP3484881.1
JAGBEF010000063.1:2949-11508
Oscillospiraceae bacterium

Acetate_kinase HKD HKD PLDc_N Ribosomal_L21p Ribosomal_L27 GTP1_OBG MMR_HSR1 RsgA_GTPase DUF1967 SASP DUF4368 Zn_ribbon_recom Recombinase Resolvase PBECR4

MBP3538304.1
JAGBDI010000033.1:1-3682
Oscillospiraceae bacterium

Mg_chelatase ? PBECR4 ? DNA_pol3_delta2 PSP1 PSP1_3rd

MBP3567586.1
JAGBCP010000011.1:149-18939
Lachnospiraceae bacterium

Sacchrp_dh_NADP Sacchrp_dh_C Ala_racemase_N Orn_DAP_Arg_deC Flg_new_2 CotH CHB_HEX_C_1 SCAB-Ig ? PBECR4 Na_H_Exchanger HTH_18 AraC_binding MatE MatE MFS_1 OAD_beta SBP_bac_8 4HB_MCP_1 HAMP MCPsignal

MBP3568588.1
JAGBCP010000049.1:28920-48210
Lachnospiraceae bacterium

DUF4293 MCPsignal PilZ Sipho_Gp157 AAA_3 AAA_lid_2 vWA BatA VWA_2 VWA_2 VWA DapB_N DAPDH_C PBECR4 BacA Receiver Trans_reg_C ABC_tran DUF2705 His-Kinase His-Kinase AraA_N AraA_central Arabinose_Iso_C ECF_trnsprt

MBP3741617.1
JAGAZB010000005.1:116361-136219
Treponema sp.

Mbeg1-like LON_substr_bdg AAA Lon_lid Lon_C BD-FAE 7TMR-DISM_7TM SpoIIE Hydrolase Glyco_hydro_10 DUF456 PBECR4 DUF1949 Impact_N DNA_topoisoIV Lig_chan Slo-like_RCK cNMPBD OLD-like_TOPRIM AAA_15 nSTAND3 Radical_SAM DUF3990

MBP3808679.1
JAGAXK010000038.1:82711-97142
Eubacterium sp.

YlxR Ribosomal_L7Ae IF2_N GTP_EFTU EF-G_D2 IF-2 GTP_EFTU_D2 RBFA DHH DHHA1 TruB_N TruB_C_2 FAD_syn Flavokinase ? PBECR4 AsnC_trans_reg HTH_AsnC-type S4 PseudoU_synth_2 Nlig-Ia DNA_ligase_aden OB_DNA_ligase HHH_2 BRCT HTS ? HTH_17 PARG_cat_microb

MBP3818038.1
JAGAXN010000157.1:1-10165
Butyrivibrio sp.

Trns_repr_metal PBECR4 ? Dynamin_N Peptidase_M48 Dynamin_N Dynamin_N Zn_ribbon_3 PDZ_2 Trypsin

MBP3899668.1
JAGAVP010000034.1:42444-52135
Candidatus Saccharibacteria bacterium

PIN TRAM Transpeptidase Transgly SYY_C-terminal tRNA-synt_1b ? ? PMM ? PBECR4

MBP5201192.1
JAGDCL010000018.1:147-4123
bacterium

PBECR4 ? Lcl_C Lcl_C Acetate_kinase

MBP5436886.1
JAGCWT010000049.1:1-12877
Treponema sp.

BE_C TP_0855_helical TP_0855_C HAMP SpoIIE tRNA-synt_1b Peptidase_M18 Ala_racemase_N Ala_racemase_C PBECR4

MBP5602417.1
JAGCTZ010000116.1:2647-18298
Treponema sp.

TP_0789-like ? HAD_2 ? ? DUF5066 LRAT PBECR4 Rick_17kDa_Anti ? ? ? AAA_16 AAA_16 B12-binding B12-binding_2 Pterin_bind S-methyl_trans

MBP5751930.1
JAGCQK010000267.1:219-8940
Treponema sp.

? Glyco_transf_8 Acyltransferase Acyltransferase Glyco_transf_8 ? PBECR4 BPD_transp_2 BPD_transp_2 ABC_tran

MBP7349322.1
JAGOGF010000150.1:356-5681
Butyrivibrio sp.

PBECR4 Aldolase_II RhaA Bac_rhamnosid_C Bac_rhamnosid6H Bac_rhamnosid Bac_rhamnosid_N

MBP8687992.1
JAGPLA010000012.1:225-8669
Bacilli bacterium

PBECR4 UPF0004 Radical_SAM ABC_membrane ABC_tran ABC_membrane ABC_tran ? ? ? ATP-synt_C

MBQ0013929.1
JAGHVH010000004.1:54-12086
Candidatus Limimonas egerieequi

PhdYeFM_antitox ? HTH_17 Fic Ribosomal_S2 EF-Ts_N EF_TS DUF2804 CitMHS PBECR4 PBP ? N_methyl Wzy_C N_methyl A24_N_bact Peptidase_A24

MBQ1175356.1
JAFOFG010000064.1:224-8611
Treponema sp.

Abi_2 HTH_11 WYL WCX EMC3_TMCO1 YtrI_N AbiH PBECR4 ODP Flavodoxin_5

MBQ1393365.1
JAFOKB010000501.1:205-2742
Lachnospiraceae bacterium

HTH_3 WYL WCX HTH_26 PBECR4

MBQ1658769.1
JAFOQX010000128.1:5168-20906
Clostridia bacterium

DAHP_synth_1 DAHP_snth_FXD SKI Sacchrp_dh_NADP Shikimate_dh_N PP-binding DHQS_C DHQ_synthase PDH_C PDH_N ProRS-C_1 HGTP_anticodon tRNA-synt_2b PBECR4 UPRTase Wzy_C Gp_dh_C Gp_dh_N ? Citrate_synt DUF7537 ?

MBQ1726674.1
JAFOQD010000232.1:1-2486
Treponema sp.

? PBECR4 TEN_YD-shell

MBQ1833965.1
JAFOTA010000248.1:1-4025
Treponema sp.

DAO Fer2_BFD Pyr_redox_2 DUF1667 PBECR4 ?

MBQ2902498.1
JAFQRZ010000032.1:14228-30836
Agathobacter sp.

DUF8351 PGA_cap iPGM_N Phosphodiest SecG OB_RNB CSD2 RNB S1 SmpB HFX_2341_N Card1_endonuc HAD_2 PBECR4 Lactamase_B SPM SDH_alpha PadR DUF2812 PHZA_PHZB DUF4352

MBQ2904125.1
JAFQRY010000020.1:3413-19329
Clostridia bacterium

DUF3656 Peptidase_U32 ZapA ? Amidohydro_2 YfbR-like Sortase Isochorismatase PBECR4 DAHP_snth_FXD DAHP_synth_1 PDH_N PDH_C DHQ_synthase DHQS_C Y1_Tnp EPSP_synthase Chorismate_synt CM_2 PDT ACT

MBQ2923759.1
JAFQSK010000226.1:20738-41396
Tyzzerella sp.

DUF2371 Amidase_2 SKI Hydrolase_like SDH_C Shikimate_dh_N DHquinase_I EFP_N EFP Elong-fact-P_C DUF5688 PBECR4 ? Cupin_2 HTH_18 SBP_bac_8 BPD_transp_1 BPD_transp_1 Glyco_hydro_43 Glyco_hydro_43 PEGA Flg_new_2 Flg_new_2 Flg_new_2 Flg_new_2 Flg_new_2

MBQ2986326.1
JAFQRJ010000010.1:67100-82614
Tyzzerella sp.

Complex1_51K SLBB Fer4_17 RnfC_N BMC BMC HTH_DeoR DeoRC DEAD DEAD_2 Helicase_C_2 LysR_substrate HTH_1 Lit FGAR-AT_linker AIRS_C GATase_5 PBECR4 RelB YafQ_toxin Spore_III_AA Spore_III_AB SpoIIIAC SpoIIIAC SpoIIIAC Spore_III_AE

MBQ3368417.1
JAFQZM010000025.1:151653-166830
bacterium

DRTGG His-Kinase Fer4_10 Fe_hyd_lg_C Fe_hyd_lg_C FeS Lcl_C ATP-synt_ab Rho_RNA_bind Rho_N ? UVR UvrB Helicase_C UvrB_3rd UvrB_inter ResIII PBECR4 ? Acyl_transf_3 Bro-N YafQ_toxin ? DUF4143 AAA_14 DRTGG

MBQ3512427.1
JAFQCI010000019.1:23624-50866
Lachnospiraceae bacterium

? ? ? DUF4869 AbiEi_4 AbiEii ? ? EAL GGDEF A_deaminase Acetylase Peptidase_S11 PBP5_C Carboxyl_trans OAD_gamma Biotin_lipoyl

MBQ3601644.1
JAFQAU010000242.1:2065-6577
Lachnospiraceae bacterium

PBECR4 Resolvase HTH_19 ? PemK_toxin Tn916-Xis Integrase_DNA Phage_int_SAM_5 Phage_integrase LMWPc

MBQ4091404.1
JAFQLG010000081.1:156-3572
Clostridia bacterium

ArdcN MPTase-PolyVal ? PBECR4

MBQ4235978.1
JAFPQE010000146.1:310-2737
Treponema sp.

? Radical_SAM PBECR4

MBQ4490825.1
JAFPZT010000277.1:1-9441
Pyramidobacter sp.

MnmE_helical TrmE_N Abhydrolase_6 Aminotran_1_2 HTH_3 PBECR4 ? ? Peptidase_M20 Macro

MBQ4497820.1
JAFQAB010000133.1:15663-27320
Spirochaetaceae bacterium

Peptidase_S9 TetR_C_8 TetR_N Methyltransf_11 EamA EamA CN_hydrolase NAD_synthase Acetylase Acetylase PBECR4 ? Acetylase Acetylase Acetyltransf_7 Acetylase Acetylase ?

MBQ4523249.1
JAFQBM010000040.1:26534-40789
Lachnospiraceae bacterium

? ? GGDEF TetR_N ? CotH Sigma70_r4_2 Sigma70_r2 PBECR4 MgtE CBS CBS MgtE_N ? DNA_alkylation PDDEXK_9 AAA-ATPase_like ? DUF3592 ?

MBQ5400669.1
JAFNSP010000139.1:194-10142
Treponema sp.

SASA SASA Citrate_synt Glyco_hydro_31_3rd Glyco_hydro_31_2nd Gal_mutarotas_2 Flavin_Reduct Lon_C Lon_lid AAA LON_substr_bdg ? PBECR4

MBQ5907287.1
JAFOCI010000039.1:207-15126
Treponema sp.

Glycos_transf_4 AICARFT_IMPCHas MGS MethyltransfD12 N6_N4_Mtase DUF1015 DNA_methylase MerR RE_EcoO109I ? PBECR4 Sigma54_AID Sigma54_CBD Sigma54_DBD Hpr_kinase_N Hpr_kinase_C PTS-HPr LexA_DNA_bind Peptidase_S24 DNA_pol3_delta PC4

MBQ5919797.1
JAFOCM010000069.1:1-2332
Selenomonadaceae bacterium

ABC_tran BCA_ABC_TP_C ABC_tran PBECR4

MBQ6400212.1
JAFRHH010000068.1:14097-24045
Clostridia bacterium

Glyoxalase Acetyltransf_7 Hydrolase AhpC-TSA Abhydrolase_11 Zn_dep_PLPC ? PBECR4 IstB_IS21 Mu-transpos_C_2 rve SH3_3 SH3_4

MBQ6530314.1
JAFRHZ010000284.1:1-2150
Clostridia bacterium

ABC_tran PBECR4 ? ?

MBQ6844302.1
JAFSFZ010000137.1:16930-26337
Agathobacter sp.

LytTR Receiver Peptidase_S41 Chromate_transp Chromate_transp MazG Acetylase Acetylase PBECR4 Acetylase Abhydrolase_1 VanZ DUF4317 DUF4317 Acetylase Acetylase NUDIX

MBQ7054366.1
JAFSDO010000182.1:1-12900
Oscillospiraceae bacterium

SLH ASL_C2 Lyase_1 Arginosuc_syn_C Arginosuc_synth Aldolase LytR_cpsA_psr ? ? PBECR4 ? SpoIIE SpoIIE_N PEPCK_N PEPCK_GTP

MBQ7477250.1
JAFSXD010000109.1:7114-18632
Selenomonadaceae bacterium

? DFP Flavoprotein RNA_pol_Rpb6 Guanylate_kin RemA-like DAP_epimerase DAP_epimerase PBECR4 CobS Aminotran_5 HicB_lk_antitox HicA_toxin GDP_Man_Dehyd dTDP_sugar_isom ABC-3

MBQ7537777.1
JAFSYN010000049.1:11827-25479
Treponema sp.

GHMP_kinases_N GalKase_gal_bdg LNT_N CN_hydrolase BioY ABC_tran CbiQ Zn_ribbon_NrdR ATP-cone Torsin Zn_Ribbon_1 PBECR4 OTCace_N OTCace TP_0437 DHH DHHA1 ? GerE Ham1p_like Flagellin_N Flagellin_C

MBQ7615591.1
JAFTDS010000171.1:214-9947
Butyrivibrio sp.

PBECR4 ? DUF3048 DUF3048_C ? HAMP His_kinase His-Kinase Receiver HTH_18 DUF3502 BPD_transp_1

MBQ7913393.1
JAFUJR010000032.1:97390-114095
Clostridia bacterium

? tRNA-synt_1b Bac_DNA_binding DUF2179 YitT_membrane Ribosomal_L9_C Ribosomal_L9_N DUF1540 PTS_EIIC_2 PBECR4 DUF1846_C DUF1846 NUDIX Adenylsucc_synt CoA_binding DAPDH_C DUF6264 Sulfatase Glyco_tranf_2_3

MBQ7932755.1
JAFUKR010000974.1:190-1821
Clostridia bacterium

Relaxase PBECR4

MBQ7955765.1
JAFUIR010000016.1:19329-32812
Lachnospiraceae bacterium

ABC2_membrane_6 ? SSF SSF GH113 DUF3221 Methyltransf_31 ? PBECR4 CoiA_N CCDC93_CC ABC_tran ABC2_membrane_3 LytTR DUF3021 His-Kinase His-Kinase Receiver Hpt MatE MatE

MBQ8039584.1
JAFUIJ010000419.1:1-2376
Lachnospiraceae bacterium

AhpC-TSA ABC_tran AAA_15 NUDIX PBECR4

MBQ8133071.1
JAFUFF010000014.1:13646-20746
Clostridia bacterium

? PBECR4 ? DUF7695 ? HAD_2 S1 HHH_9 HHH_3 Tex_YqgF Tex_central_region Tex_N ? HGSNAT_cat

MBQ8264488.1
JAFTTV010000202.1:186-3648
Oscillospiraceae bacterium

PBECR4 DDAH_eukar LRRs

MBQ8316335.1
JAFTPY010000342.1:1-7927
Lachnospiraceae bacterium

PBECR4 ? Aminotran_1_2 Esterase Glyco_hydro_10 MarR TonB_N Glyco_hydro_10 TonB_N

MBQ8398125.1
JAFTOI010000037.1:3464-23225
Clostridia bacterium

DNA_gyraseB_C Toprim DNA_gyraseB His-Kinase RemA-like SMC_N DNA_pol3_beta_3 DNA_pol3_beta_2 DNA_pol3_beta Bac_DnaA_C Hda_lid Bac_DnaA DnaA_N Phosphodiest Metalloenzyme ? PBECR4 DUF6809 NAD_Gly3P_dh_C NAD_Gly3P_dh_N SBP_bac_8 HMGL-like HCS_D2 Glyco_hydro_39 MFS_1 MFS_1 PHP

MBQ8416719.1
JAFTMU010000346.1:499-8853
Clostridia bacterium

HTH_31 DUF6514 DUF3671 ? ? ? ? PBECR4 MFS_2 Glyco_hydro_2_N Glyco_hydro_2 Glyco_hydro_2_C

MBQ8510574.1
JAFUQU010000041.1:8535-22950
Clostridia bacterium

MFS_1 MFS_1 ? SpoVT_C MazE_antitoxin ? Polysacc_deac_1 Penicillinase_R Peptidase_M56 PBECR4 B12-binding B12-binding_2 ? Transketolase_C Transket_pyr Transketolase_N ? Phage_lysozyme SKA1

MBQ8665433.1
JAFUSB010000018.1:2238-13307
Lachnospiraceae bacterium

? ? ? ? ? Receiver LytTR SPM PBECR4 PadR FTSW_RODA_SPOVE ? GGDEF DUF6363

MBQ8699044.1
JAFURW010000512.1:1-1578
Schwartzia sp. (in: firmicutes)

TipAS PBECR4

MBQ8782767.1
JAFTWE010000014.1:88632-104681
Clostridia bacterium

Phe_tRNA-synt_N tRNA-synt_2d tRNA_bind B3_4 B5 tRNA_synthFbeta FDX-ACB CTP_transf_1 DAGK_cat YegS_C AAA AAA_assoc_2 MgsA_C Hydrolase_3 UPF0758_N RadC PBECR4 DUF2691 MatE MatE DUF4364 PHP DUF378 NAD_binding_8 Calcineurin

MBQ8788219.1
JAFTWF010000011.1:1-9312
Oscillospiraceae bacterium

PBECR4 Resolvase Recombinase Zn_ribbon_recom Cass2 HTH_18 Big Cadherin-like PQQ_2 ?

MBQ8803067.1
JAFTWA010000022.1:38631-56816
Tyzzerella sp.

Fe-ADH_2 ? DUF4867 Lipase_GDSL_2 Pribosyltran HD_4 RelA_SpoT TGS RelA_AH RelA_RIS ACT_4 PBECR4 PBECR4 Lactamase_B Radical_SAM tRNA-synt_His N-OB tRNA-synt_2 LUD_dom GATase_6 SIS SIS PTS_EIIC PTS_IIB PTS_EIIA_2

MBQ8803750.1
JAFTWA010000042.1:39311-54964
Tyzzerella sp.

DLH ADH_N ADH_zinc_N PfkB PfkB AAA-ATPase_like PDDEXK_9 Penicillinase_R Peptidase_M56 PBECR4 ApbE NusG_II Hpre_diP_synt_I RuvA_N HHH_5 RuvA_C RuvB_N AAA_lid_4 WHD_RuvB ZapA Peptidase_U32 DUF3656 Peptidase_U32

MBQ8857432.1
JAFTYT010000083.1:991-16875
Lachnospiraceae bacterium

HTH_3 Cupin_2 ABC_tran TOBE_2 BPD_transp_1 BPD_transp_1 SBP_bac_8 Gly_kinase ? AlaDh_PNT_N AlaDh_PNT_C PBECR4 ? TM1266-like FecCD ABC_tran TM1266-like Radical_SAM Fer4_NifH Oxidored_nitro

MBQ8857725.1
JAFTYT010000107.1:168-14684
Lachnospiraceae bacterium

CW_binding_2 CW_binding_2 HTH_3 LysM Glyco_hydro_18 PBECR4 Fer4_17 Aldo_ket_red SDH_beta ACT SDH_alpha DUF554 tRNA-synt_1g tRNA-synt_1g Anticodon_3 tRNA_bind DUF6465 CW_binding_2 CW_binding_2 CW_binding_2

MBQ8982417.1
JAFUAW010000037.1:96317-109946
Lachnospiraceae bacterium

Acylphosphatase GTP_EFTU EF-G_D2 EFG_III EFG_IV EFG_C NYN_YacP ? PBECR4 MSC PolyA_pol PolyA_pol_RNAbd tRNA_NucTran2_2 Spore_coat_YutH PEGA PEGA GGDEF EAL ? TatD_DNase

MBQ9111117.1
JAFTQJ010000067.1:15059-32613
Oscillospiraceae bacterium

? Citrate_synt SpoIID Peripla_BP_3 GGDEF ? Sigma70_r4_2 Sigma70_r2 TPP_enzyme_C Fer4_16 EKR POR PFOR_II POR_N PBECR4 GH94_b-supersand Glyco_hydro_94 Glyco_hydro_65C

MBQ9119041.1
JAFTQM010000026.1:511-8358
Lachnospiraceae bacterium

PBECR4 ? YbjN HTH_3 Glyco_hydro_88 Glyco_hydro_106 ? tRNA-synt_1b

MBQ9205489.1
JAFUDX010000007.1:32042-48610
Treponema sp.

SLBB HTH_3 Peptidase_M24 Creatinase_N Epimerase EAL ABC_tran_CTD ABC_tran ABC_tran_Xtn ABC_tran ATPase_2 DUF234 PBECR4 ? ? YccF YccF ? SH3_3 GTP_EFTU GTP_EFTU_D2 GTP_EFTU_D3 Ribosomal_S10

MBQ9206081.1
JAFUDX010000014.1:38666-53685
Treponema sp.

DUF645 PNPase SBP_bac_11 BPD_transp_1 BPD_transp_1 ABC_tran TOBE_2 Flg_new LRRs PBECR4 DUF3800 ? Zip Zip MatE MatE ABC_membrane ABC_tran ABC_membrane ABC_tran DUF454

MBQ9206104.1
JAFUDX010000014.1:62269-69051
Treponema sp.

PBECR4 Acetylase Abhydrolase_3 Methyltransf_11 LCM DUF4143 AAA_14 Methyltransf_11 Flg_new

MBQ9282870.1
JAFUFU010000045.1:90443-102732
Treponema sp.

? HisKA_3 Receiver GerE BCA_ABC_TP_C ABC_tran ? Zn_Ribbon_1 MamF_MmsF ? PBECR4 PBECR4 MCPsignal FeS Fe_hyd_lg_C Fer4 Fer4 IMS IMS_C ? Thioredoxin_2 CNNM CBS CBS CorC_HlyC CNNM CBS CorC_HlyC

MBQ9423800.1
JAFTBZ010000401.1:77-4991
Pyramidobacter sp.

TetR_N PBECR4 ? PDDEXK_3 Nitroreductase ? Peptidase_M3_N

MBQ9611668.1
JAFTFD010000084.1:13-2863
Lachnospiraceae bacterium

PhageMin_Tail CHASE3 PBECR4 ?

MBR0031963.1
JAFSJW010000060.1:19758-34941
Treponema sp.

ABC_tran tRNA-synt_2b HGTP_anticodon CtpB_N-like PDZ_6 Peptidase_S41 PUA_4 Methyltrans_RNA Glyco_tran_WecG AP_endonuc_2 DNA_topoisoIV PBECR4 Impact_N DUF1949 DUF4172 Fic AAA_15 ? HTH_3 HTH_3 ?

MBR0091661.1
JAFSLB010000234.1:1-4004
Lachnospiraceae bacterium

RepA_N Cys_rich_VLP Relaxase MobC NikA-like PBECR4

MBR0261943.1
JAFSOQ010000115.1:1394-10208
Selenomonadaceae bacterium

STAS PBECR4 HTH_26 MethyltransfD12 MethyltransfD12 RE_AlwI ? ? Radical_SAM MmeI_C

MBR1443142.1
JAFUUG010000244.1:491-1521
Bacillota bacterium

PBECR4 AlkZ-rel

MBR1477535.1
JAFUVF010000039.1:61-8789
Lachnospiraceae bacterium

? G5 VanW PG_binding_4 ? ? HTH_31 Glycos_transf_2 Epimerase DUF4422 PBECR4 C2185-like_N DegT_DnrJ_EryC1 ?

MBR1553113.1
JAFUWC010000133.1:10445-25015
Schwartzia sp. (in: firmicutes)

AzlC AzlD Radical_SAM LytR_cpsA_psr HhH-GPD Glyco_tranf_2_5 Glycos_transf_2 DegT_DnrJ_EryC1 PBECR4 WbqC Acetylase Pyridox_ox_2 SDF 5_nucleotid_C Calcineurin ? RUBY_RBDX Rubrerythrin

MBR1559385.1
JAFUWR010000107.1:1-16251
Clostridia bacterium

EcoRI_methylase GmrSD_N HNH Pyr_redox_2 Oxidored_FMN TAT_signal HTH_1 LysR_substrate HTH_3 Lyase_1 ASL_C2 PBECR4 Mannitol_dh_C EFG_C EFG_IV EFG_III EF-G_D2 GTP_EFTU Ribosomal_S7 Ribosom_S12_S23 Ribosomal_L7Ae HD_5 HD MgtC

MBR1695681.1
JAFUZC010000696.1:1-2995
Selenomonas sp.

? POTRA_2 ShlB PBECR4

MBR1742278.1
JAFVAA010000476.1:235-2835
Lachnospiraceae bacterium

PBECR4 Peptidase_M78 ?

MBR1747831.1
JAFVAC010000088.1:1-26208
Clostridia bacterium

ArdcN MPTase-PolyVal MutS_I NrS1-1_pol-like_HBD ? MobL T4SS-DNA_transf Big_13 Big_13 Big_13 Big_13 Big_13 Big_13 Big_13 Big_13 Big_13 Big_13 Big_13 Big_13 Big_13 T4SS_pilin PBECR4 ? ? TrbL_4 ?

MBR2048837.1
JAFVMW010000080.1:499-14504
Oscillospiraceae bacterium

? Polysacc_deac_1 2Fe-2S_thioredx Complex1_51K SLBB NADH_4Fe-4S Fer4 Fer4 Fer2_4 Fer4_20 Pyr_redox_2 Fer4_7 FemAB FemAB Ala_racemase_N Ala_racemase_C PBECR4 NusG_II Ribosomal_L21p Peptidase_Prp Ribosomal_L27 GTP1_OBG MMR_HSR1 DUF1967 ParB_N HTH_ParB

MBR2660057.1
JAFWEJ010000003.1:1-14134
Clostridia bacterium

DUF6883 DUF4926 NikA-like TnpV AAA_15 ABC-ATPase OLD-like_TOPRIM AAA_19 ? PBECR4 Sigma70_r2 Sigma70_r4_2 ? Transposase_20 DEDD_Tnp_IS110 ? HTH_31

MBR2765685.1
JAFWDX010000318.1:1-5146
Blautia sp.

PBECR4 IPPT IPT MutL_C DNA_mis_repair HATPase_c_3 PDDEXK_9 AAA-ATPase_like

MBR3624036.1
JAFXOC010000518.1:320-5331
Selenomonadaceae bacterium

eIF-1a Ribosomal_L36 Ribosomal_S13 Ribosomal_S11 Ribosomal_S4 S4 RNA_pol_A_bac RNA_pol_A_CTD Ribosomal_L17 PBECR4 Ribosomal_L17 ?

MBR3752893.1
JAFXCU010000165.1:1-6740
Ruminiclostridium sp.

Rhodanese HSP90 HATPase_c_3 ? ? PBECR4 RecG_dom3_C Helicase_C DEAD RecG_wedge

MBR4031174.1
JAFWXH010000003.1:23955-39965
Clostridia bacterium

TRAM_2 Radical_SAM UPF0004 His-Kinase His-Kinase HAMP Trans_reg_C Receiver TetR_N ? ? ? PBECR4 Methyltransf_11 Bin3 ? Phage_int_SAM_1 Phage_integrase ? N6_N4_Mtase ?

MBR4061126.1
JAFXAZ010000102.1:2844-14591
Lachnospiraceae bacterium

CTP_transf_like Scy Gate S4 PseudoU_synth_2 Hydrolase Radical_SAM_N Radical_SAM DUF3362 ? PBECR4 DUF2651 Acetylase Hydrolase_3 Methyltransf_23 Hydrolase_3 Cyclase LCM Say1_Mug180 SpoV_N

MBR4341911.1
JAFXXN010000040.1:1-2717
Lachnospiraceae bacterium

Phage_integrase PBECR4 ? DUF2334

MBR4345142.1
JAFXXN010000196.1:32222-42076
Lachnospiraceae bacterium

ABC_tran FtsX FtsX MacB_PCD IU_nuc_hydro HicB_lk_antitox Y1_Tnp PDDEXK_9 AAA-ATPase_like MurJ PBECR4 ?

MBR4387448.1
JAFXWC010000073.1:15442-34448
Treponema sp.

DUF8052 CstA CstA ADH_Fe_C Fe-ADH Acetate_kinase ? ? ? PBECR4 GSIII_N Gln-synt_C Gln-synt_C-ter DUF6198 ApbA Peptidase_M16_C Peptidase_M16_C Peptidase_M16 Nitroreductase EstA_Ig_like RF-1

MBR4776284.1
JAFZKS010000046.1:39-7991
Lachnospiraceae bacterium

? ? Glycos_transf_2 Hydrolase PBECR4 ?

MBR4823389.1
JAFZJX010000024.1:5808-13026
Spirochaetaceae bacterium

HepT-like Polbeta HicB PBECR4 ? ? ANKs ANKs DUF7738 UDG ? DUF4160 DUF2442

MBR4959433.1
JAFZET010000025.1:1-5394
Clostridia bacterium

HTH_ParB ParB_N DUF4368 Zn_ribbon_recom Recombinase Resolvase ? PBECR4 Sigma70_r4_2 Ada3 HTH_3

MBR5220170.1
JAFYTT010000116.1:1-16755
Clostridia bacterium

HTH_3 PEPCK_GTP PEPCK_N SBP_bac_1 YjeF_N Carb_kinase PBECR4 DUF4838 Glyco_hydro_106 PadR DUF2812 Sigma70_r4 Sigma70_r3 Sigma70_r2 His-Kinase STAS SLH SLH

MBR5294225.1
JAFYOO010000272.1:1-8143
Oscillospiraceae bacterium

Peptidase_M42 AMPT PBECR4 Sigma70_r4 Sigma70_r3 Sigma70_r2 Sigma70_r1_2 Sigma70_r1_1 GTP_EFTU GTP_EFTU_D2 RF3_C EFG_C LepA_C Radical_SAM HemN_C malic Malic_M ABC_tran_CTD

MBR5317908.1
JAFYOW010000283.1:1-6645
Lachnospiraceae bacterium

? DUF4275 HTH_3 ? ? DUF981 HTH_3 PBECR4 Spore_III_AA

MBR5506480.1
JAFYUP010000017.1:4185-25748
Clostridia bacterium

? SBP_bac_3 SBP_bac_3 DUF389 BPD_transp_1 ABC_tran Virulence_RhuM DUF6809 PBECR4 GFO_IDH_MocA_C3 GFO_IDH_MocA HTH_18 Cupin_2 ? AraC_binding HTH_18 DUF4962 HepII_C Cu_amine_oxidN1 SLH SLH SLH SLH

MBR5566357.1
JAFYVJ010000075.1:19185-31899
Roseburia sp.

DegV ? QueT AI-2E_transport AMP_N Peptidase_M24 adh_short Arg_tRNA_synt_N tRNA-synt_1d DALR_1 PBECR4 ? ? AAA_23 ABC-ATPase Sigma70_r2 Sigma70_r4_2 zf-HC2 SHOCT DUF4275

MBR5570761.1
JAFYVL010000075.1:4036-20210
Oscillospiraceae bacterium

AraC_binding HTH_18 YmdB Calcineurin AAA_27 SMC_N MgtC TrkA_N TrkA_C TrkA_N TrkA_C TrkH PBECR4 HTH_3 SHOCT SBP_bac_8 BPD_transp_1 BPD_transp_1 TOBE_2 ABC_tran SpoU_methylase

MBR5578163.1
JAFYWD010000097.1:1-5056
Lachnospiraceae bacterium

DUF285 DUF285 Big_13 ? PBECR4

MBR5798880.1
JAFZDQ010000021.1:48517-63414
Lachnospiraceae bacterium

Spore_YabQ DivIC SpoIIE_N SpoIIE ATP_bind_3 TilS_C Pribosyltran FtsH_ext AAA AAA_lid_3 Peptidase_M41 Alpha-amylase_N Alpha-amylase Alpha-amylase PBECR4 HTH_18 RelB HTH_11 WYL WCX Cass2 Cass2 DUF3788 DUF3795 DUF6144

MBR5965718.1
JAFZLA010000045.1:13176-35556
Treponema sp.

Beta_helix PDDEXK_2 LRRs LRRs PBECR4 ATPase_2 HxlR DUF234 Sigma54_AID Sigma54_CBD Sigma54_DBD Ribosomal_S30AE Hpr_kinase_N Hpr_kinase_C PTS-HPr LexA_DNA_bind Peptidase_S24 ?

MBR6153475.1
JAFXZQ010000068.1:629-12343
Treponema sp.

Semialdhyde_dh Semialdhyde_dhC_1 ? NAD_synthase CN_hydrolase Peptidase_S41 YfhO Glyco_hydro_10 Dala_Dala_lig_C Dala_Dala_lig_N GGDEF PBECR4 DUF2281 PIN ?

MBR6296651.1
JAFYDJ010000071.1:345-18058
Treponema sp.

? TetR_C_33 TetR_N Abhydrolase_1 ? Epimerase Fer4_6 Peptidase_U32 PBECR4 ? AAA-ATPase_like PDDEXK_9 PDDEXK_2 SSB DUF7954 DUF7955 HNH GmrSD_N EcoRI_methylase

MBR6510673.1
JAFYLM010000016.1:1-8418
Phascolarctobacterium sp.

AICARFT_IMPCHas Radical_SAM Peptidase_M20 BATS Radical_SAM RNase_T PBECR4 ? Peptidase_M20

MBR6701039.1
JAFXHN010000082.1:273-7549
Bacillota bacterium

Eno-Rase_FAD_bd Enoyl_reductase Eno-Rase_NADH_b RelB HI0933_like DUF1648 Fumerase Fumerase_C Pyr_redox_2 ?

MBS1477525.1
JABMAG010000001.1:5777-23287

Angelakisella sp.

Relaxase ? ? Sigma70_r4_2 Sigma70_r2 ? Peptidase_C39_2 ? PBECR4 SpoIID ? Sigma70_r4_2 Sigma70_r2 PAS_GdpP GGDEF_GdpP DHH DHHA1 Ribosomal_L9_N Ribosomal_L9_C DnaB DnaB_C ATP_bind_3 TilS TilS_C

MBS4460949.1
JAGYWM010000001.1:1-11235
Tuanshanicoccus yangjingiae

Y1_Tnp PBECR4 MatE MatE RelB Methyltransf_11 DUF4298 UvrD-helicase UvrD_C PcrA_UvrD_tudor Nlig-Ia DNA_ligase_aden OB_DNA_ligase DNA_ligase_ZBD HHH_5 HHH_2 BRCT CamS

MBS5037739.1
JAGZKN010000017.1:764-10564
Fusobacterium sp.

AIRS_C AIRS Acylphosphatase Ppx-GppA Aminoglyc_resit Peptidase_M48 MORN_2 MORN_2 MORN_2 MORN_2 MORN_2 MORN_2 ? PBECR4 IstB_IS21 ? ? ?

MBS5038296.1
JAGZKN010000032.1:126-8271
Fusobacterium sp.

Bac_DNA_binding HicA_toxin HicB_lk_antitox ? PBECR4 PBECR4 Receiver Trans_reg_C HAMP His-Kinase His-Kinase DUF3450 Peptidase_M19 EIIA-man PTSIIB_sorb EII-Sor

MBS5038530.1
JAGZKN010000041.1:4547-18212
Fusobacterium sp.

? Autotransporter Bac_DNA_binding Bac_DNA_binding PBECR4 CSD FtsX MacB_PCD ABC_tran YknX_C Beta-barrel_YknX BSH_YknX ? Thiolase_N Thiolase_C Acyl-CoA_dh_N Acyl-CoA_dh_M Acyl-CoA_dh_1

MBS5575124.1
JAGZCH010000006.1:51099-61305
Bacillota bacterium

? ? ? DUF6291 HicB ? ? PBECR4 ? SBP_bac_8 BPD_transp_1 BPD_transp_1 TOBE_2 ABC_tran PseudoU_synth_2 S4 YceD

MBS5586922.1
JAGZCI010000350.1:1-3214
Clostridiales bacterium

Colicin_V URO-D PBECR4 ABC2_membrane_6

MBS5922130.1
JAHAJG010000126.1:1-7434
Clostridium perfringens

PBECR4 ? ? Holin_BhlA DUF3810

MBS7194682.1
JAGZPA010000001.1:30659-45901
Eubacterium sp.

CitMHS CitMHS CitMHS ? HPPK FolB Pterin_bind HD Mur_ligase_C Mur_ligase_M PBECR4 FMN_red HTH_26 Fic DUF3298 PdaC Cu_amine_oxidN1 Cu_amine_oxidN1 YqeY Ribosomal_S21 Alpha-amylase_C Alpha-amylase Alpha-amylase CBM_48 GlgB_N

MBS7360137.1
JAHAYC010000347.1:170-2507
Oscillospiraceae bacterium

PBECR4 MFS_1

MBX4257882.1
JAIFNQ010000055.1:1-11368
Enterococcus lactis

HMA Cu-oxidase_3 Cu-oxidase Cu-oxidase_2 Receiver Trans_reg_C His-Kinase His-Kinase ? DUF1541 DUF1541 DDE_Tnp_ISL3 HTH_23 Zn_ribbon_ISL3 PBECR4 Transposase_mut SHOCT YNCE Cytochrom_D1 His-Kinase

MBY5033912.1
JAIMFC010000002.1:108128-120170
Streptococcus gallolyticus

? ? DUF1366 ? ? Phage_holin_6_1 CHAP PBECR4 ? SocA_Panacea DUF1132 Paratox RecR_HhH RecR_ZnF Toprim_4 RecR_C ? Dala_Dala_lig_N Dala_Dala_lig_C

MCB6806666.1
JAJCGS010000003.1:7633-33271

bacterium MSK18_59

SocA_Panacea ? ? ? ? UPF0547 ? PBECR4 Big DUF6558 DUF6558_C ? CCDC39 CCDC39 Peptidase_S74 ? ? PTR

MCC2176694.1
JAJEPX010000013.1:46660-56907

Agathobaculum butyriciproducens

Toprim DUF4093 ? ? HipA_C Phage_integrase Arm-DNA-bind_4 Phage_integrase Phage_int_SAM_3 PBECR4 Bro-N Peptidase_S24 HTH_3 DUF739 ? ? DUF2207_C HTH_3

MCD7805984.1
JAJQGR010000052.1:1-4504
Lachnospiraceae bacterium

PBECR4 ASD1_dom Alpha-L-AF_C ? ? EamA EamA

MCD7954166.1
JAJQEO010000001.1:17066-39062
Lachnospiraceae bacterium

Mitofilin ATLF DUF624 Uma2 tRNA-synt_1 Anticodon_1 DUF5915 Phosphorylase Glyco_hydro_3 Glyco_hydro_3_C Fn3-like Mem_trans PBECR4 Lipase_GDSL_2 MFS_2 Glyco_hydro_43 CBM_6 ? ? HTH_18 AraC_binding Methyltransf_1N DNA_binding_1

MCD7959548.1
JAJQEI010000043.1:2247-18218
Ruminococcus sp.

LRRs DUF4368 Zn_ribbon_recom Recombinase Resolvase ? NikA-like MobC Relaxase TP_0813_N ResIII Helicase_C PBECR4 PBECR4 ? TnpV He_PIG Glug ? ? ParB_N ParA-Soj-NTPase

MCD7967849.1
JAJQEG010000467.1:1-9501
Clostridiaceae bacterium

? PBECR4 PAP2 His-Kinase His-Kinase HAMP Trans_reg_C Receiver Methyltransf_11 ? HTH_18 AraC_binding Phage_integrase Phage_int_SAM_3 Arm-DNA-bind_4

MCD8023134.1
JAJQDM010000388.1:1-12905
Lachnospiraceae bacterium

ABC_tran NIL BPD_transp_1 Lipoprotein_9 FAD_binding_4 FAD-oxidase_C Aminotran_1_2 ATP-grasp GATase_4 PBECR4 FtrD-like HMA DsbD_2 ThiF Cys_Met_Meta_PP

MCD8026170.1
JAJQDK010000076.1:1-8452
Clostridiales bacterium

Asp_decarbox Flavoprotein DFP PBECR4 ? DUF218 Fe_hyd_lg_C Fer4_6 Fer4 DUF951 PCRF RF-1 Sua5_yciO_yrdC Sua5_C CoaE

MCD8098960.1
JAJQCF010000001.1:165-9086
Oscillospiraceae bacterium

SurA_N_3 Rotamase_3 EmrE PBECR4 Acetylase DUF401 TetR_N TetR_C_8 Desulfoferrodox Desulfoferrod_N RUBY_RBDX Rubrerythrin RUBY_RBDX G3P_acyltransf KH_dom-like MMR_HSR1 MMR_HSR1

MCD8131967.1
JAJQBK010000058.1:32833-44294
Lachnospiraceae bacterium

SH3_3 SH3_3 Lactamase_B HTH_3 OMPdecase BPD_transp_1 ABC_tran AAA_13 SBP_bac_3 PBECR4 PK PK_C HicA_toxin HicB_lk_antitox Pribosyltran ? DUF6142 AIRC

MCF0246107.1
JABUSF010000006.1:191643-209705
Ileibacterium sp.

Antibiotic_NAT GAF TPRs BPD_transp_1 Glycos_transf_2 ? SRP54_N SRP54 SRP_SPB ? Ribosomal_S16 KH_KhpA-B RimM PRC_RimM tRNA_m1G_MT ? LRRs DUF285 DUF285

MCF0259966.1
JABUSE010000048.1:20511-30494
Erysipelotrichaceae bacterium

Antibiotic_NAT GAF_2 ? BPD_transp_1 Glycos_transf_2 ? SRP54_N SRP54 SRP_SPB PBECR4 Ribosomal_S16 KH_KhpA-B RimM PRC_RimM tRNA_m1G_MT Peptidase_M15_4

MCG1667425.1
JAINPZ010000001.1:335809-345166
Staphylococcus epidermidis

HTH_Tnp_4 HTH_3 HTH_3 ? ? ? Phage_int_SAM_3 Phage_integrase PBECR4 Ribosomal_S18 SSB Ribosomal_S6 Glyco_hydro_25 ? YchF-GTPase_C MMR_HSR1 DUF951

MCH5192606.1
JAFLUI010000006.1:2644-17804
Oscillospiraceae bacterium

? ? GH3 GH3_M GH3_C B12-binding Radical_SAM SUKH-3 B12-binding Radical_SAM ? PBECR4 MCPsignal PP_kinase_C PP_kinase_C_1 PP_kinase PP_kinase_N GntR ABC_tran ? ABC2_membrane_5 Rce1-like

MCH5281333.1
JAFLSW010000017.1:4201-14996
Lachnospiraceae bacterium

DUF3006 IMS_C IMS_HHH IMS Peptidase_C26 ? ? ? ACT_8 PBECR4 DUF1848 GGDEF MNHE MrpF_PhaF PhaG_MnhG_YufB MbhD MbhE MnhB

MCI5892110.1
JALEJW010000023.1:792-13212
Clostridiales bacterium

NTP_transferase ATP_bind_3 Cu_amine_oxidN1 CHAP SH3_3 ? MPTase-PolyVal HTH_26 PBECR4 HTH_3 ? ? ? Phage_int_SAM_3 Phage_integrase ? SocA_Panacea

MCI6186659.1
JALFAW010000112.1:212-12635
Spirochaetia bacterium

? ? AAA_15 ABC_tran FtsK_gamma ? LRAT PBECR4 HTH_3 ? Dynamin_N IFT57 BLOC1_2 Dynamin_N Dynamin_N ?

MCI6269278.1
JALEZM010000052.1:26707-43131
Clostridiales bacterium

ABC_tran ABC_tran BPD_transp_2 BPD_transp_2 BSH_CusB BSH_YknX RND-MFP_C ABC_tran MacB_PCD FtsX BSH_CusB BSH_RND Beta-barrel_YknX PBECR4 HD TraI_2 N-OB Peripla_BP_4 ABC_tran ABC_tran BPD_transp_2 ? RUBY_RBDX Rubrerythrin Rubredoxin

MCI6272130.1
JALEZD010000014.1:6954-21586
Erysipelotrichaceae bacterium

SpaA SpaA ? DUF4116 DUF4116 DUF4116 DUF4116 Zn_ribbon_DnaG Toprim_2 ArdcN MPTase-PolyVal ? ? PBECR4 ? ? ? ? TraC-like DUF6096 ? DUF3226 Peptidase_M23

MCI6700145.1
JALETT010000041.1:1984-11300
Solobacterium sp.

PBECR4 Glyco_hydro_1 Glyco_hydro_1 Peptidase_M20 ABC_tran ABC_tran BPD_transp_1 SBP_bac_3 ToxN_toxin GGDEF TPRs

MCI7040520.1
JALFMK010000001.1:178-8640
Lachnospiraceae bacterium

PBECR4 TetR_N adh_short adh_short AP_endonuc_2 Penicillinase_R Peptidase_M56 ? ABC_tran ABC-ATPase

MCI7057808.1
JALFLU010000045.1:1-9831
Mollicutes bacterium

Glycos_transf_1 ? ? PBECR4 ? ? S1 HHH_9 HHH_3 Tex_YqgF Tex_central_region Tex_N Peptidase_C69

MCI7279456.1
JALEWV010000072.1:1680-11803
Faecalibacterium prausnitzii

RicinB_lectin_2 RicinB_lectin_2 ? ? Nitroreductase Acetylase Trp_repressor DJ-1_PfpI PBECR4 FAA_hydrolase TatA_B_E CRLF3_N TatA_B_E TatC ROK ? DUF6773

MCI7330007.1
JALFII010000010.1:599-21934
Selenomonadaceae bacterium

X25_BaPul_like X25_BaPul_like X25_BaPul_like Alpha-amylase_N Alpha-amylase SLH Calcineurin 5_nucleotid_C Acid_phosphat_B ? S1-P1_nuclease PBECR4 Acid_phosphat_B YfhO dCache_1 HAMP MCPsignal ABC_tran NIL VraH BPD_transp_1 Lipoprotein_9 FBPase_2

MCI7343827.1
JALFTV010000115.1:4825-11917
Fusobacterium necrophorum

DUF3310 HTH_23 ? Terminase_6N Portal_Mu Phage_Mu_F Ntox50 ? Phage_tail_S PBECR4

MCI8295493.1
JAAVXS010000029.1:7497-23954
Lachnospiraceae bacterium

? FecR PNPase AICARFT_IMPCHas IMP_cyclohyd PTS_IIB AMMECR1 LigB PBECR4 2-Hacid_dh_C Ldh_2 TctA TctB TctC HTH_1 LysR_substrate Cellulase

MCI8521258.1
JAAWBY010000210.1:5238-16249
Clostridia bacterium

? ? ? ? ? ? DUF3848 PBECR4 ? DUF6906 Sigma70_r2 Prok-JAB ThiF DUF6094 ? ?

MCI8741074.1
JAAWFO010000003.1:7027-24414
Lachnospiraceae bacterium

? PDZ_2 Trypsin MutS_V MSSS Smr Receiver Trans_reg_C PBECR4 LysR_substrate HTH_1 DUF3798 ABC_tran ABC_tran BPD_transp_2 BPD_transp_2 Peptidase_M20 Peptidase_M20 LysR_substrate HTH_1

MCI8774729.1
JAAWFY010000030.1:147-10765
Lachnospiraceae bacterium

? CD1107-like CD1107-like Collagen ? Toprim Topoisom_bac DUF5710 DUF5710 NikA-like MobC PBECR4 Relaxase

MCI8822657.1
JAAWGX010000020.1:38240-46475
Lachnospiraceae bacterium

ABC_tran PBECR4 Receiver LytTR SPOB_a HATPase_c_5 DUF5643 DUF4179 Sigma70_r4_2 Sigma70_r2 FTSW_RODA_SPOVE HAAS PadR DUF2284

MCI8979426.1
JAAWJG010000023.1:6928-13446
Clostridia bacterium

? ? ? ? ? ? DUF3848 PBECR4 ? DUF6906 Sigma70_r2

MCI8980220.1
JAAWJG010000118.1:69-5918
Clostridia bacterium

RGL11_C RGI_lyase HTH_5 Ribosomal_S21 YqeY PBECR4 Phage_integrase HTH_26 ? ?

MCI8987900.1
JAAWJF010000110.1:96-7210
Lachnospiraceae bacterium

DUF1648 ? PBECR4 Ribosomal_L21p Peptidase_Prp Ribosomal_L27 GTP1_OBG MMR_HSR1 DUF1967 CRS1_YhbY CTP_transf_like HD

MCI9128256.1
JAAWLJ010000111.1:48-3954
Eubacterium sp.

? PBECR4

MCI9335109.1
JAAWOX010000142.1:217-7138
Lachnospiraceae bacterium

HATPase_c_5 SPOB_a LytTR Receiver ABC_tran ABC_tran ? MobL PBECR4

MCI9407482.1
JAAWPZ010000007.1:52744-66054
Clostridia bacterium

dUTPase ROK Put_DNA-bind_N CoA_binding SNF SNF 2Fe-2S_thioredx 2Fe-2S_thioredx Complex1_51K SLBB NADH_4Fe-4S Fer4_10 Fer2_4 NADH-G_4Fe-4S_3 Fer4_7 Fe_hyd_lg_C Fe_hyd_SSU PBECR4 Pyr_redox_2 Fer4_20 HIT ? RuvX DUF1292 HTH_3 Ribosomal_S2

MCI9465753.1
JAAWQU010000002.1:120181-137500
Ruminiclostridium sp.

Ala_racemase_N SepF DivIVA tRNA-synt_1 Anticodon_1 zf-FPG_IleRS Peptidase_A8 S4 PseudoU_synth_2 Hydrolase_3 PBECR4 Thiolase_N Thiolase_N Thiolase_C ? CMD CMD Glyco_tranf_2_3 Methyltrans_SAM PUA_3 RNase_Y_N KH_1 HD ?

MCI9479494.1
JAAWRB010000048.1:1-16439
Lachnospiraceae bacterium

NTP_transferase Hexapep_GlmU NTP_transferase Hexapep_GlmU Phage_P4_cII RelB SKI ? AAA_11 AAA_12 DUF2726 PBECR4 Amino_oxidase Sigma70_r2 Sigma70_r4_2 ? SNF SNF Pan_kinase ECF_trnsprt

MCI9564916.1
JAAWSL010000004.1:51312-65168
Eubacterium sp.

ABC_tran Receiver Trans_reg_C His-Kinase His-Kinase Abhydrolase_3 MerR_1 MerR-DNA-bind GyrI-like GyrI-like Phage_integrase Phage_int_SAM_1 ? DUF305 4HBT ABC_tran ABC_tran Glyoxalase_2 NTP_transf_2 AadA_C Synaptojanin ?

MCI9650620.1
JAAWTP010000018.1:304-17956
Lachnospiraceae bacterium

BPD_transp_1 Alpha_L_fucos Alpha_L_fucos SBP_bac_1 ? His-Kinase His_kinase dCache_1 PBECR4 Glyco_hydro_28 DUF3502 SBP_bac_1 BPD_transp_1 BPD_transp_1 ? DUF624 DUF3502

MCJ7689265.1
JALHVS010000550.1:167-2121
Clostridiaceae bacterium

dNK PBECR4 ?

MCL1983345.1
WRJV01000317.1:1-15289
Clostridiales bacterium

Ribosomal_L11 Ribosomal_L1 Ribosomal_L10 RL10_C Ribosomal_L12_N Ribosomal_L12 Wzy_C PBECR4 ? RNA_pol_Rpb2_1 RNA_pol_Rpb2_3 RNA_pol_Rpb2_45 RNA_pol_Rpb2_6 RNA_pol_Rpb2_7 RNA_pol_Rpb1_1 RNA_pol_Rpb1_2 RNA_pol_Rpb1_3 RNA_pol_Rpb1_4 RNA_pol_Rpb1_5 RNA_pol_Rpb1_5 Ribosom_S12_S23 Ribosomal_S7 GTP_EFTU EF-G_D2 EFG_III EFG_IV EFG_C

MCL2077033.1
WRLY01000001.1:266783-297057
Oscillospiraceae bacterium

? Transglutaminase TctC PemK_toxin RelB MBG_2 MBG_2 MBG_2 MBG_2 ? PBECR4 ? Kei1 ZnR SAICAR_synt RUBY_RBDX Rubrerythrin Big_14 HTH_3 HTH_3

MCL2286196.1
WQTQ01000197.1:6672-18261
Bacillota bacterium

PBECR4 Phosphorylase Cu_amine_oxidN1 Glyco_hydro_18 OGG_N HhH-GPD PhoU PhoU Na_Pi_cotrans Na_Pi_cotrans CN_hydrolase NAD_synthase Cu_amine_oxidN1 MICAH DegV

MCL2499436.1
WRDO01000007.1:32545-54378
Defluviitaleaceae bacterium

FAD_binding_2 URO-D FliG_N FliG_M FliG_C GlcNAc_2-epim Flavodoxin_5 Fer4_7 Fer4_7 ArsC HicB_lk_antitox PBECR4 ? ? Glycos_transf_2 Glyphos_transf SLFN_AlbA_2 HATPase_c_4 Glycos_transf_2 YkvP_N Glyco_trans_1_2 Glyco_trans_1_2 Glyco_trans_1_4 Glyco_trans_1_4

MCL2840642.1
WRAH01000015.1:43976-55763
Defluviitaleaceae bacterium

MOFRL DUF4147 GntP_permease F420_ligase DUF218 LytTR ? ? PBECR4 HTH_3 MraZ MazE_antitoxin HTH_3 TPRs ? ? ?

MCM1048915.1
JAMPHY010000011.1:45386-69434
Clostridiales bacterium

GMPPB_C PAS PAS GGDEF Sortase PDDEXK_2 LRRs LRRs LRRs LRRs LRRs Flg_new_2 LRRs LRRs LRRs LRRs Peptidase_S8 PBECR4 GntR FCD Iso_dh ABC_tran_CTD ABC_tran_Xtn ABC_tran ABC_tran_Xtn ABC_tran ? YjeF_N Carb_kinase Ala_racemase_N Ala_racemase_C PemK_toxin

MCM1059779.1
JAMPHS010000016.1:6398-26419
Eubacterium sp.

DUF4316 GGDEF ? OrfB_IS605 Cas12f1-like_TNB ? ? LPD25 WH_1 DUF8437 Helicase_dom Helicase_C PBECR4 SSB ? Peptidase_C39 BACON Peptidase_C39_2 ? DUF4367 Sigma70_r4_2 Sigma70_r2

MCM1090372.1
JAMPHH010000012.1:6144-17937
Muribaculum sp.

AsnC_trans_reg Aminotran_1_2 SpoU_methylase VanZ MFS_2 ? Imm48 PBECR4 SMI1_KNR4 ? HTH_26 ? HAD_2 ABC-ATPase ABC_tran ABC_tran_Xtn ABC_tran ?

MCM1136046.1
JAMPGS010000088.1:1-13542
Clostridium sp.

MFS_1 AbiEi_4 AbiEii MatE MatE Beta-AFase-like_GH127_cat Glyco_hydro127M Glyco_hydro127C MerR_1 TipAS GmrSD_N GmrSD_C DUF4268 PBECR4 HsdM_N N6_Mtase

MCM1144660.1
JAMPGJ010000061.1:67-15739
Lachnoclostridium sp.

Glyco_hydro_43 CBM_6 Glyco_hydro_3 Glyco_hydro_3_C Fn3-like ? ? DUF6718 PBECR4 HTH_18 Glyco_hydro_1 Glyco_hydro_1 MFS_2 Glyco_hydro_2_N Glyco_hydro_2_N Glyco_hydro_2 Glyco_hydro_2_C Bgal_small_N ? DUF4153

MCM1156398.1
JAMPGI010000050.1:1407-10663
Roseburia sp.

PIN MazE_antitoxin ? CopG_antitoxin BrnT_toxin Lactamase_B_3 ? PBECR4 Acetylase Phage_int_SAM_1 Phage_integrase ? Amidase_2 Phage_lysozyme DUF2589 ? DUF2589 Exonuc_VII_L

MCM1188469.1
JAMPFT010000002.1:151666-168821
bacterium

RF-1 PCRF ? SEC-C SecA_SW P-loop_SecA P-loop_SecA SecA_DEAD APH PNPase Methyltransf_11 Pectinesterase Pectinesterase PBECR4 Zn_Ribbon_1 Zn_Ribbon_1 ? FliD_C phiKZ_IP Nitroreductase LytTR Receiver LacI Peripla_BP_3

MCM1215708.1
JAMPGK010000014.1:141-13174
Lachnospiraceae bacterium

Dala_Dala_lig_C Dala_Dala_lig_N GGDEF GAF ? PBECR4 MatE MatE ChlI AAA_25 Zn_ribbon_LapB ? ClpB_D2-small AAA_2 AAA_lid_9 AAA Clp_N GntR SH3_3 SH3_3 NRDD

MCM1234973.1
JAMPFL010000303.1:192-5701
Ruminococcus flavefaciens

NikA-like PBECR4 Relaxase Relaxase_C ? Fungal_TACC

MCM1264130.1
JAMPEU010000083.1:315-5712
Butyrivibrio sp.

HTH_3 Receiver Acetylase ? DUF2383 ABC_membrane ABC_tran ABC_membrane

MCM1268406.1
JAMPEN010000065.1:1-7669
Bacteroidales bacterium

? HATPase_c_5 LytTR Receiver PBECR4 ApbA_C ApbA MNHE MrpF_PhaF PhaG_MnhG_YufB MbhD MbhE MnhB Oxidored_q2

MCM1328918.1
JAMPDU010000028.1:4392-20337
Ruminococcus sp.

Glyco_hydro_43 Pan_kinase ECF_trnsprt Polbeta ? MazE_antitoxin SpoVT_C SBP_bac_8 PBECR4 PBECR4 ToxN_toxin MgtE CBS CBS MgtE_N CotH CotH DUF4956 VTC QueF

MCM1540155.1
JAMPAC010000001.1:571464-587973
Blautia sp.

PARG_cat_microb HhH-GPD LysM Glyco_hydro_18 MTHFR MoxR-AAA ? VWA_CoxE PBECR4 tRNA-synt_1b SYY_C-terminal Zn_Ribbon_1 LRR_14 MS_channel_1st_1 MS_channel_1st_1 MS_channel_1st_1 SpoIVA_ATPase SpoIVA_middle SpoIVA_C DUF2142 PNPase dCMP_cyt_deam_1

MCM1560571.1
JAMPAD010000040.1:16841-34440
Butyrivibrio sp.

Cyclophil_like2 Fer4_9 Aldo_ket_red FtsX MacB_PCD FtsX ABC_tran AMP-binding CBAH HTH_1 LysR_substrate PBECR4 ? Peptidase_S8 CspB_prodomain Peptidase_M18 MPI_cupin_dom PMI_typeI_cat Cupin_2 NTP_transferase Epimerase GDP_Man_Dehyd

MCM1578814.1
JAMOZU010000150.1:1-5515
Ruminococcus sp.

PBECR4 PBECR4 Alpha-amylase Malt_amylase_C DUF1653 Rubrerythrin RUBY_RBDX HTH_11 WYL WCX Pan_kinase

MCP1462035.1
JALJWJ010000001.1:4044969-4058140
Bacillus amyloliquefaciens

LysE AraC_binding Telomerase_RBD HTH_18 ? SpoIID ? RapH_N TPRs TPRs ? PBECR4 ? Abhydrolase_1 Sugar_tr MFS_1 Staph_reg_Sar_Rot DUF4467 MaoC_dehydratas YjbR

MCQ2478376.1
JAKSQL010000075.1:1-5377
Clostridia bacterium

DUF2953 Peptidase_M20 Creatinase_N Peptidase_M24 Peptidase_M20 PBECR4

MCQ2550706.1
JAKSSK010000002.1:29500-44165
Clostridia bacterium

Na_H_antiporter GerE Fer4_21 Aldo_ket_red ? ? cobW CobW_C cobW DUF1980_C PBECR4 ? DUF4430 ? CbiQ ABC_tran ABC_tran ECF-ribofla_trS HTH_3 Cupin_2

MCQ2596568.1
JAKSTG010000002.1:125273-137739
Treponema sp.

Toprim Topoisom_bac Toprim_Crpt ? ? ? ? Claudin_2 ? PBECR4 ? NikA-like TrbL TrbI CagX VirB8 ?

MCR4718029.1
JAIKVQ010000006.1:1-7883
Bacillota bacterium

FGGY_N FGGY_C Amidohydro_1 Ceramidase_alk ? Phage_integrase Phage_int_SAM_3 PBECR4 ? DUF6398

MCR5125487.1
JAILEW010000020.1:44743-60182
Treponema sp.

S-AdoMet_synt_C S-AdoMet_synt_M S-AdoMet_synt_N AMPK1_CBM MatE MatE ? TPRs TPRs TPRs RNaseH-CATRA+Caspase HTH_3 LRRs LRRs LRRs PBECR4 PfkB PyrI_C PyrI OTCace OTCace_N PDDEXK_2 HTH_3 YxzE ?

MCR5338350.1
JAILJH010000188.1:1-5506
Lachnospiraceae bacterium

? fn3 Peptidase_C1 PBECR4 HD

MCR5554849.1
JAILMC010000033.1:224-2226
Bacteroidales bacterium

PBECR4 TPRs LPAM_1

MCT4584089.1
JAOARY010000029.1:49075-56424
Peptostreptococcaceae bacterium

? HAT1_C_fung mRNA_stabil ? ? ? ? PBECR4 ArdcN Peptidase_M78 LPD25 TTRAP ? NikA-like ? ? ? ?

MCX4298595.1
JAPKXB010000094.1:57-14610
Lachnospiraceae bacterium

? ? RdRP ? PBECR4 HTH_19 ? YomN PhageMin_Tail Filament CCDC89 Asp_protease_2 ?

MDC7290506.1
JANSWJ010000023.1:7345-22537
Blautia schinkii

DctQ DctM DUF386 Bac_rhamnosid6H Bac_rhamnosid_C NMT1 ADH_zinc_N ADH_N Peripla_BP_3 LacI PBECR4 Acetylase Acetyltransf_CG ? ARMT1-like_dom ABC_tran OB_MalK TOBE_2 GGDEF_2 HTH_30 ABC_tran

MDD3205543.1
JAQUYA010000035.1:1-11936
Lachnospiraceae bacterium

ABC_tran CPSase_sm_chain GATase CPSase_L_D1 CPSase_L_D2 CPSase_L_D3 CPSase_L_D1 CPSase_L_D2 MGS PBECR4 ? ? LuxS PNPase UCP028175 PGM_PMM_I PGM_PMM_II PGM_PMM_III PGM_PMM_IV DEAD Helicase_C

MDD4729923.1
JAQVZQ010000334.1:1-3861
Dysgonamonadaceae bacterium

Zn_ribbon_Top1 ? PBECR4 Recombinase

MDD6076832.1
JAQXLG010000008.1:1-1910
Clostridiales bacterium

adh_short_C2 ? PBECR4

MDD6119816.1
JAQXKL010000017.1:495-13560
Selenomonadaceae bacterium

? MatE MatE YjfB_motility TSCPD ? HTH_3 HigB-like_toxin PBECR4 ABC_tran BPD_transp_1 SBP_bac_11 MoCF_biosynth MOSC Mob_synth_C Radical_SAM MoeA_C MoCF_biosynth MoeA_N MoCF_biosynth

MDD6237818.1
JAQXHX010000002.1:258-11501
Oscillospiraceae bacterium

GARS_N GARS_A GARS_C N-OB tRNA-synt_2 PBECR4 Flavodoxin_1 DUF3793 LRRs SLH SLH SLH Voltage_CLC GATase_7 Pribosyltran Gln-synt_N Gln-synt_C ANTAR

MDD6481824.1
JAQXZD010000074.1:7179-20049
Lachnospiraceae bacterium

Sod_Cu NUDIX DUF2383 Coat_F CE2_N Lipase_GDSL_2 ABC_tran ABC2_membrane MerR_1 GyrI-like PBECR4 HMA E1-E2_ATPase Hydrolase HTH_5 Transglutaminase DUF4358 Methyltransf_11 PGA_cap

MDD6489847.1
JAQXZA010000104.1:24454-36588
Clostridia bacterium

bPH_2 bPH_2 bPH_2 DUF815 Peripla_BP_2 PG_binding_1 PNPase PBECR4 ? HTH_3 ? DNA_gyraseA_C DNA_gyraseA_C DNA_gyraseA_C DNA_gyraseA_C DNA_gyraseA_C DNA_topoisoIV YcxB ? 4HBT_2

MDD6491354.1
JAQXYZ010000048.1:174-8250
Bacillota bacterium

PBECR4 ? Tn916-Xis Integrase_DNA Phage_int_SAM_3 Phage_integrase MraY_sig1 Glycos_transf_4 MurD-like_N Mur_ligase_M Mur_ligase_C FTSW_RODA_SPOVE EPSP_synthase

MDE6128351.1
JAIDBG010000329.1:1-2662
Lachnospiraceae bacterium

Mem_trans PBECR4 Pyridox_ox_2

MDE6388354.1
JAIDVO010000024.1:30131-40641
Lachnospiraceae bacterium

? ? DUF2726 ? HTH_19 HVO_2718 DUF2080 Zn_ribbon_3 PBECR4 ? Resolvase Recombinase Zn_ribbon_recom

MDE6607375.1
JAIDRR010000279.1:1-3046
Lachnospiraceae bacterium

PBECR4 tRNA-synt_1 Anticodon_1

MDE6620238.1
JAIDRM010000206.1:156-6275
Lachnospiraceae bacterium

PDDEXK_2 ? PBECR4 ? ? ? DUF6783 SIS HTH_6

MDE6830248.1
JAIEKW010000726.1:433-1540
Lachnospiraceae bacterium

PBECR4 Radical_SAM

MDE6846912.1
JAIDOR010000250.1:1-9876
Lachnospiraceae bacterium

DUF2726 ? HTH_3 HTH_3 Zn_Ribbon_1 PBECR4 ? Resolvase Recombinase Zn_ribbon_recom Mn_catalase CotJB CotJA ABC_tran DrrA1-3_C ABC2_membrane_3 DUF7088 ABC_transp_aux

MDE6933619.1
JAIEJR010000178.1:1-11994
Oscillospiraceae bacterium

rve_2 Xan_ur_permease DUF3795 3D G5 Pept_tRNA_hydro PBECR4 Aldo_ket_red Flavodoxin_4 SLH SLH SLH Hexapep Hexapep FMN_red Abhydrolase_6 HTH_1 LysR_substrate HTH_26 ?

MDE7210465.1
JAIEEJ010000257.1:409-2187
Lachnospiraceae bacterium

? Mur_ligase_C

MDE7444152.1
JAIEAM010000002.1:67753-89837
Lachnospiraceae bacterium

GGDEF GAF MCPsignal MCP-like_PDC_1 HATPase_c_5 LytTR Receiver HTH_3 Pyr_redox_2 Pyr_redox_2 Fer4_20 GXGXG Glu_synthase Glu_syn_central GATase_2 PBECR4 Rce1-like HAD_2 S1 S1 S1 RUBY_RBDX Flavin_Reduct ABC_tran ABC_tran_Xtn ABC_tran Phosphorylase Peripla_BP_3 LacI

MDE7446478.1
JAIEAM010000056.1:45289-61716
Lachnospiraceae bacterium

TetR_N Glyco_hydro_2_N Glyco_hydro_2 Glyco_hydro_2_C Glyco_hydro2_C5 DUF6937 DUF6938 MFS_2 Glyco_hydro_36N Melibiase Glyco_hydro_36C ECF_trnsprt DUF6033 PBECR4 TraX ? ? YjbR FMN_red ? DUF6351

MDF2544329.1
JAQZBN010000067.1:1799-9723
Herbinix sp.

? ? ? Methyltransf_13 Sigma70_r2 ? ? PBECR4 ? HTH_3 Peptidase_M78 TENA_THI-4 ? Methyltransf_11 HEPN ?

MDG3141466.1
JAKTNK010000001.1:207734-225203
Streptococcus suis

Prophage_tail Glucosaminidase CHAP Collagen DUF859 DUF7365 Phage_holin_1 Amidase_5 ZoocinA_TRD ? Striatin PBECR4 Peptidase_S24 HTH_3 DeoRC Rib_5-P_isom_A Metalloenzyme PNPase Voltage_CLC PNPase Cas_Csm6_HEPN

MDK0980848.1
JAROAL010000031.1:1-16726

Clostridium perfringens

Choline_bind_3 Choline_bind_3 SH3_3 YcxB ? ? ? Resolvase PBECR4 GKRP_SIS_N SIS GKRP-like_C PTS_EIIB PTS_EIIC MupG_N MupG_C HTH_6 SIS NUMOD3 ? ?

MDK0981338.1
JAROAL010000078.1:13-4616
Clostridium perfringens

ParB_N ParB_N ParA-Soj-NTPase PBECR4 ? ? ? Sigma70_r4 Holin_BhlA

MDM8111836.1
JAUDBV010000008.1:7695-23050
Phascolarctobacterium faecium

AcetylCoA_hydro AcetylCoA_hyd_C MM_CoA_mutase MmgE_PrpD_N MmgE_PrpD_C HTH_3 ? Hydrolase_3 SLH Porin_5 PBECR4 SLH ? BSH_RND Beta-barrel_RND_2 ABC_tran MacB_PCD FtsX ? CTP_transf_like

MDM8212631.1
JAUDCW010000002.1:148124-159538
Enterococcus hirae

IstB_IS21 HTH_28 PBSX_XtrA ? ? DUF722 ? PBECR4 Cupin_2 DUF6796 DUF998 ECF_trnsprt Fe_hyd_SSU Fe_hyd_lg_C Fer4_Nqo3 NADH-G_4Fe-4S_3 Fer2_4 Fer4_20 Pyr_redox_2 Fer4_20 NADH_4Fe-4S FeoA FeoA

MDO4155462.1
JAUNJC010000008.1:10748-27826
Oscillospiraceae bacterium

TrwB_AAD_bind Peptidase_M48 OmpA ? ? ? ? PBECR4 ? ? ? STY-kinase PP2C_2 VWA_2 ?

MDO4469512.1
JAUNDO010000011.1:47533-70300
Bacillota bacterium

Oxidored_FMN Pyr_redox_2 2-Hacid_dh_C MFS_1 MFS_1 ADH_zinc_N ADH_N FGGY_N FGGY_C ABC2_membrane_3 Apolipoprotein ABC2_membrane_3 ABC2_membrane_3 ATG17_like ABC2_membrane_3 PBECR4 HMA E1-E2_ATPase Hydrolase FeoA FeoB_N FeoB_Cyto Gate FeoB_C Gate HTH_5 Glyco_H_20C_C Glyco_hydro_20 MatE MatE CntK_N

MDO4509659.1
JAUNCM010000022.1:16582-30039
Lachnospiraceae bacterium

ResIII ? SLFN_AlbA_2 HATPase_c_4 HTH_IclR ? ? HTH_3 ? PBECR4 PIN ? DUF3795 TraX Na_H_Exchanger Peptidase_C26 Citrate_synt

MDO4516697.1
JAUNCL010000014.1:19218-33578
Bacillota bacterium

FtsX FtsX EamA EamA HSP90 HATPase_c_3 DUF6726 ? ? ? PBECR4 RecG_dom3_C Helicase_C DEAD RecG_wedge Gate Gate MazE_antitoxin DZR_2 RsmI_C TP_methylase MTS NUDIX

MDO5407990.1
JAUNPU010000021.1:41304-64247
Eubacteriales bacterium

Acetyltransf_7 Acetylase Bmp ABC_tran ABC_tran BPD_transp_2 BPD_transp_2 ABC_tran UvrA_inter UvrA_DNA-bind AAA_16 ABC-ATPase UPF0236 PBECR4 HAD_2 Trans_reg_C BTAD GGDEF DUF7601 DUF7601 DUF11 SpaA Gram_pos_anchor Sortase ?

MDO5787412.1
JAUNWI010000011.1:7030-20538
Phascolarctobacterium sp.

? ? LbH_EIF2B ? DUF4160 SLH ? PBECR4 SLH DUF2442 DUF2178 HTH_3 AAA_14 DUF4143 AAA_14 DUF4143 JetD_C

MDR1018832.1
JAISGP010000142.1:19597-37856
Lachnospiraceae bacterium

FGGY_C FGGY_N Transketolase_C Transket_pyr Transketolase_N ? HTH_3 Peripla_BP_1 FtsX MacB_PCD ABC_tran PBECR4 Tautomerase tRNA_U5-meth_tr TRAM HD N-OB HhH-GPD OGG_N MutS_V MSSS Smr ? YkzU

MDR2833070.1
JAITWV010000185.1:1-4226
Streptococcaceae bacterium

GramPos_pilinD1 PBECR4 FTSW_RODA_SPOVE

MDU2049276.1
JAWDVK010000051.1:11555-17943
Clostridium perfringens

HTH_3 COA8 ? HTH_28 Phage_int_SAM_1 Phage_integrase ? Resolvase HTH_28 PBECR4

MDU4714862.1
JAWGBU010000047.1:99-12674
Gemella haemolysans

N-OB tRNA-synt_2 DnaD_N DnaB_2 HhH-GPD Peptidase_A8 PBECR4 Methyltransf_1N DNA_binding_1 Formyl_trans_N Formyl_trans_C NusB RsmF-B_ferredox Methyltr_RsmB-F RlmN_N Radical_SAM PP2C_2 PP2C STY-kinase DUF6548 PASTA PASTA PASTA GIY-YIG UvrC_M UVR UvrC_RNaseH Antimicrobial_7 UvrC_RNaseH_dom HHH_5

MDU6691665.1
JAWHBI010000030.1:6825-20461

Clostridium perfringens

? GIY-YIG ? DUF4003 ? Resolvase HTH_7 ToxN_toxin PBECR4 ? ? HNH Terminase_4 TerL_ATPase TerL_nuclease Phage_portal Peptidase_S78

MDY5330496.1
JAXFID010000054.1:39116-55142
Anaerovibrio sp.

RmlD_sub_bind NeuB Acetylase C2185-like_N DUF6165 Methyltransf_31 ? NTP_transferase PBECR4 GDP_Man_Dehyd DegT_DnrJ_EryC1 Epimerase BCCT NTP_transf_3 Choline_kinase Sulfatase

MDY5341831.1
JAXFHV010000023.1:615-14592
Faecousia sp.

? ? ? ? ? PBECR4 adh_short_C2 MatE MatE Cons_hypoth698 HTH_1 LysR_substrate ? MMPL MMPL DUF308 DUF308 DUF308

MDY6334815.1
JAXGAV010000254.1:1-3177
Lachnospiraceae bacterium

SpoU_methylase Sigma70_r2 Sigma70_r4_2 PBECR4 Ribosomal_L31 DUF1385

MEA4998065.1
JAYFOV010000007.1:22713-45482
Candidatus Limiplasma sp.

GT2_TM_C Glycos_transf_2 Asp_Glu_race Acetylase Na_H_Exchanger PapZ_C RapZ-like_N MurB_C FAD_binding_4 CorA PBECR4 ? Tubulin_2 ? ? ABC_tran ABC_membrane ABC_tran ABC_membrane DUF6119

MEA5145494.1
JAYFNL010000294.1:1-2819
Candidatus Limiplasma sp.

RapZ-like_N MurB_C FAD_binding_4 CorA PBECR4

MED9780501.1
JAXJLE010000032.1:156-5059
Peptococcaceae bacterium

? Big Big Ig_3 Flg_new_2 SLH SLH SLH PBECR4 GIY-YIG 5_3_exonuc_N

MED9780542.1
JAXJLE010000034.1:1-9077
Peptococcaceae bacterium

DUF6291 ? ? ? HTH_26 PBECR2 ? PBECR4 Big

MED9968057.1
JAXJKY010000114.1:23902-30763
Blautia sp.

DUF6472 ? ? ATG22 ATG22 ? RNPP_C TPRs HTH_3 PBECR4

MEE0347367.1
JAXJDD010000032.1:1850-18346
Lachnospiraceae bacterium

Glyco_hydro_1 PTS_EIIA_1 PTS_EIIC PTS_EIIB SIS HTH_6 DUF6449 ABC_tran GntR PBECR4 FMN_red Nitroreductase Hemerythrin MCPsignal Mce4_CUP1 HAMP dCache_1 DUF4519 CstA CstA ? ?

MEE0366410.1
JAXJBT010000499.1:5084-21370
Oscillospiraceae bacterium

CTD7 MC3 DUF3732 DUF1492 ? DUF6017 HTH_36 ? PBECR4 ? ? HTH_18 GGDEF_2 LRR_RI_capping SBP_bac_8 DUF3502 BPD_transp_1 BPD_transp_1 MR_MLE_N MR_MLE_C

MEE0547403.1
JAXIZO010000136.1:350-8593
Peptococcaceae bacterium

PBECR4 Cu_amine_oxidN1 Flg_new_2 Pel9A-like_beta_helix Cu_amine_oxidN1 PPC rve_2 rve HTH_21 HTH_23 HTH_28 HTH_28 HTH_28

MEE1013411.1
JAXJVM010000098.1:7383-22415
Clostridia bacterium

His-Kinase DNA_gyraseB Toprim DNA_gyraseB_C ? Fer4_21 GidB PBP5_C Peptidase_S11 WD40_RLD WD40_RLD YkuD PBECR4 tRNA-synt_1c Anticodon_2 tRNA-synt_1g tRNA-synt_1g Lin1244_N SLH SLH DUF6062

MEE1154064.1
JAXJTR010000051.1:21312-31266
Acutalibacteraceae bacterium

? DUF3991 Toprim_2 HTH_3 HTH_36 HTH_36 ? DUF6710 Resolvase PBECR4 RelB ? Phage_integrase Phage_int_SAM_3 ? DUF6075 Zn_Tnp_IS91 ?

MEE1219081.1
JAXJSN010000062.1:1054-16368
Ruminococcus sp.

Thymidylate_kin LPG_synthase_C Acetyltransf_9 DJ-1_PfpI 5-FTHF_cyc-lig YceG Peptidase_U32 Peptidase_U32_C PBECR4 tRNA-synt_2c tRNA_SAD DHHA1 ? DUF951 PCRF RF-1 Sua5_yciO_yrdC Sua5_C CoaE SLT

MEE1243979.1
JAXJRF010000230.1:1-5748

Frisingicoccus sp.

GMPPB_C ? GGGtGRT PBECR4 Sigma54_AID Sigma54_CBD Sigma54_DBD tRNA-synt_2c tRNA_SAD

MEE1250777.1
JAXJRM010000310.1:1-2470
Lachnospiraceae bacterium

AAT PBECR4

MEE1268806.1
JAXJQR010000089.1:185-17567
Treponema sp.

? WYL WCX AAA AAA_lid_3 ? ? Microp_apicomplexa_13 ? PBECR4 ? DDE_Tnp_1_6 ? AMP-binding AMP-binding_C_3 Glyco_hydro_3 DTW Sulfate_transp STAS

MEE3313442.1
JAZAUW010000029.1:8100-24502
Treponema sp.

? DAHP_synth_1 DAHP_snth_FXD DUF937 ? Bmp DUF5312 PBECR4 MgsA_C AAA_assoc_2 AAA ? TP_0126 THF_DHG_CYH THF_DHG_CYH_C HTH_26 Gp49 Rce1-like

MEE3315004.1
JAZAUW010000208.1:1-4144
Treponema sp.

? PBECR4 ?

NBH28819.1
QXWO01000105.1:328-9505
Lachnospiraceae bacterium

? AbiH PBECR4 HTH_3 ? Resolvase Recombinase Zn_ribbon_recom LPD39

NBK94159.1
QZDX01000027.1:17695-31252
bacterium 1XD21-13

? AAA_11 AAA_12 DUF2726 PBECR4 Amino_oxidase HTH_11 PRD PTS_EIIA_2 PTS_EIIA_2 PTS_IIB EIIC-GAT PTE Aldolase

NQJ22663.1
JABKXV010000043.1:10355-17395
Streptococcus suis

PBECR4 Cons_hypoth95 CTP_transf_like PDZ_2 Lon_C YutD-like RlmN_N Radical_SAM VanZ PALP

NQP03945.1
JABLME010000001.1:75164-100587
Streptococcus suis

? T4SS-DNA_transf Maff2 TrbL_2 PrgI HerA-FtsK P-loop_TraG Peptidase_M23 Phage_lysozyme2 CHAP PBECR4 Adhesin_P1_N GbpC AgI_II_C2 AgI_II_C2 AgI_II_C2 Antigen_C Gram_pos_anchor TSP3_bac TSP3_bac PLP_IMCC1989 N6_Mtase WH_1 DUF8437 Helicase_dom Helicase_C RVT_1 RVT_1 Intron_maturas2 AI2M-like_HNH ? DUF5962

NYS34084.1
JACBXT010000352.1:4-513
Streptococcus danieliae

PBECR4

OKZ98121.1
MNSC01000048.1:2896-17545

Coprobacillus sp. CAG:235_29_27

60KD_IMP Jag_N KH_KhpA-B R3H Mem_trans G5 VanW WWE TrmE_N MnmE_helical ? MS_channel_1st MS_channel_2nd MS_channel_3rd PBECR4 ? Meth_synt_2 ? DNA_methylase DNA_methylase ? ?

OTX40469.1
NFCR01000037.1:1-6082

Bacillus thuringiensis serovar malayensis

? ? PBECR4 Rep_1 ? HTH_3 Resolvase Recombinase

OXM14779.1
NMUQ01000002.1:1234112-1251975
Paenibacillus herberti

Lipase_GDSL_2 Glyco_hydro_38N ROK ? HTH_18 AraC_binding HTH_AraC AraC_binding Bac_rhamnosid-like_N Bac_rhamnosid6H PBECR4 Cu_amine_oxidN1 ABC_membrane ABC_tran DUF1854 Fic MazE_antitoxin STK_08120-like ABC_tran LytTR

PWM31541.1
QAKV01000032.1:10188-18841
Clostridiales bacterium

? ? ? ? Myxo_TraA_N Radical_SAM OrfB_IS605 Cas12f1-like_TNB ?

PWM72366.1
QAKB01000026.1:2733-7555
Oscillospiraceae bacterium

? DUF6291 ? HTH_17 ? HTH_3 Arm-DNA-bind_4 Phage_int_SAM_3 Phage_integrase PBECR4

RGC56952.1
QVFE01000009.1:18132-41231
Agathobaculum butyriciproducens

Radical_SAM ParA Nitro_FeMo-Co DUF6587 Mur_ligase_M Mur_ligase_C STAS His-Kinase Sigma70_r2 Sigma70_r3 Sigma70_r4 PBECR4 DUF4186 ? ? Pribosyltran Xan_ur_permease N_methyl ?

RKI20037.1
RAYF01000169.1:464-1769
bacterium D16-36

PBECR4 S-AdoMet_synt_N S-AdoMet_synt_M

RKI81757.1
RAYM01000023.1:8629-23589
bacterium 1xD42-87

? ? HTH_19 Pps Pps ? ? ZnR PBECR4 Resolvase Recombinase Zn_ribbon_recom HTH_24 Transpeptidase MraY_sig1 Glycos_transf_4 MurD-like_N Mur_ligase_M Mur_ligase_C FTSW_RODA_SPOVE EPSP_synthase POTRA_1 FtsQ_DivIB_C

SCJ41366.1
FMGW01000006.1:117044-134699
uncultured Eubacterium sp.

ChlI Mg_chelatase Mg_chelatase_C DNA_processg_A Toprim Topoisom_bac Zn_ribbon_Top1 Zn_ribbon_Top1 ? GmrSD_N Ribosomal_S2 EF-Ts_N EF_TS PBECR4 Acetylase ABC_tran ABC2_membrane MatE MatE OpuAC BPD_transp_1 ABC_tran

SDG85071.1
FNCM01000014.1:29441-44916
Selenomonas sp. WCT3

Complex1_30kDa NiFeSe_Hases Complex1_49kDa Complex1_49kDa LdpA_Fe-S-bd Oxidored_q6 PG_binding_1 3D Fer4_7 Fe_hyd_lg_C Fe_hyd_SSU Ni_hydr_CYTB ? PBECR4 BATS Radical_SAM Radical_SAM BPD_transp_1_N BPD_transp_1 OppC_N BPD_transp_1 ABC_tran oligo_HPY ABC_tran oligo_HPY SBP_bac_5

SDP26712.1
FNJQ01000011.1:43358-56072
Selenomonas ruminantium

MatE MatE MS_channel_1st MS_channel_2nd MS_channel_3rd NRDD Fer4_12 Usp Usp PALP ACT PBECR4 Flagellin_C Extensin_1 HTH_3 HTH_3 LMWPc SIS HTH_6 ?

SDX06165.1
FNOC01000042.1:20-7828
Lachnospiraceae bacterium KHCPX20

Big fn3 ? PBECR4 ? Flavin_Reduct

SFG25359.1
FOPH01000004.1:84705-103633
Oribacterium sp. WCC10

FliE MCPsignal T4SS_LegC2C7 4HB_MCP_1 DUF4422 C2185-like_N LicD ? ToxN_toxin DUF4422 PBECR4 ? Epimerase UDPG_MGDP_dh_C UDPG_MGDP_dh UDPG_MGDP_dh_N DUF4422 C2185-like_N Hydrolase_like TOD1_MUCI70 Glycos_transf_1

SHT59061.1
FSAB01000086.1:462-10153
Mycobacteroides abscessus subsp. abscessus

Hydrolase E1-E2_ATPase HMA HTH_5 ? ParA-Soj-NTPase MobA_MobL DUF3847 ? PBECR4 T4SS-DNA_transf

SUN47852.1
UHFG01000004.1:322926-336094
Streptococcus dysgalactiae subsp. dysgalactiae

DUF859 Gp10_C DUF1366 CD1375-like ? Phage_r1t_holin ? Glucosaminidase CHAP SH3_5 PBECR4 Paratox FTSW_RODA_SPOVE HAD_2 His-Kinase DNA_gyraseB Toprim DNA_gyraseB_C EzrA HAD DUF1694

SUN48923.1
UHFG01000004.1:666526-677390

Streptococcus dysgalactiae subsp. dysgalactiae

DUF1617 ? DUF1366 ? Phage_r1t_holin ? Glucosaminidase CHAP SH3_5 PBECR4 Paratox GntR UTRA UPF0122 SRP54_N SRP54 SRP_SPB FAD_binding_8 NAD_binding_1 Peptidase_S24 HTH_3 GFO_IDH_MocA GFO_IDH_MocA_C3

TWS99285.1
VOHL01000001.1:562563-578159

Streptococcus cuniculipharyngis

Prophage_tail CBM_4_9 Gp58 ? DUF1366 CD1375-like Rav1p_C Phage_holin_6_1 Amidase_2 SH3_3 PBECR4 HTH_1 LysR_substrate Peptidase_A8 S4 PseudoU_synth_2 Pribosyltran Xan_ur_permease DUF1694 Enolase_N Enolase_C

UTI88160.1
CP099817.1:834584-845423
Mammaliicoccus sciuri

? DUF7646 ? Terminase_2 Encapsidation_CP3 Sigma70_r4 ? PBECR4 ? DUF2785 PhzC-PhzF DUF7689 PRK KAP_NTPase UPF0227

UYJ00273.1
CP107213.1:1512230-1524057
Faecalibacterium prausnitzii

Fic NUDIX RicinB_lectin_2 RicinB_lectin_2 ? Acetylase Trp_repressor DJ-1_PfpI PBECR4 FAA_hydrolase TatA_B_E TatA_B_E TatC ? ABC_tran ABC_membrane Ala_racemase_N

UYJ47113.1
CP107199.1:462859-485851
Lachnospiraceae bacterium

CAT_RBD PRD PRD SIS HTH_6 SIS HTH_6 Glyco_hydro_4 Glyco_hydro_4C PTS_EIIC PTS_EIIB PTS_EIIA_1 DDE_Tnp_1 DDE_Tnp_1 PBECR4 ? DUF4349 ThrE_2 ThrE LysR_substrate HTH_1 Aminotran_1_2 MatE MatE

UYJ47994.1
CP107199.1:1526192-1543638
Lachnospiraceae bacterium

Polysacc_deac_1 RuvB_N AAA_assoc_2 MgsA_C Rho_N Rho_RNA_bind ATP-synt_ab PGM_PMM_I PGM_PMM_II PGM_PMM_III PGM_PMM_IV ABC_trans_CmpB Phage_integrase Phage_integrase Phage_int_SAM_4 PBECR4 MreB_Mbl OB_YrrC HHH_5 HHH_RecD2 AAA_19 SH3_13 UvrD_C_2 DZR_2 Pribosyltran Ribosomal_L33 SecE NusG KOW Ribosomal_L11_N Ribosomal_L11

WP_149293517.1
NZ_CP036073.1:4574101-4589056
Bacillus wiedmannii

MIP EmrE HTH_3 Cupin_2 PspC Amidohydro_3 Xan_ur_permease GerE PBECR4 AAA_15 OLD-like_TOPRIM GEMI5_RBS Sel1 ? ? ? ?

WP_250735099.1
NZ_JAGRZT010000001.1:51755-69017
Staphylococcus aureus

Phage_RBD_prop BppU_N XkdV_N DUF2977 Phage_XkdX DUF2951 Phage_holin_1 CHAP Amidase_2 SH3_5 PBECR4 MarR Glyoxalase_3 ? FemAB ACR_tran ACR_tran MspA_staph EAD9

WP_261814610.1
NZ_CAOKTW010000008.1:102054-116827
Streptococcus bouchesdurhonensis

MoCF_biosynth CinA_KH CinA CinA Amidase_2 Choline_bind_3 Choline_bind_3 Choline_bind_1 HTH_3 ? Peptidase_M78 DUF3368 PBECR4 YSIRK_signal ? ? DUF1542 DUF1542 DUF1542 DUF1542 SLATT ? ?

WP_237927077.1
NZ_JAJPGH010000002.1:18821-35986
Bacillus sp. UTDS19-33BHI26

HMA HMA Pyr_redox_2 Pyr_redox_dim MerR_1 MerR-DNA-bind MerB HTH_15 MerB ? DDE_Tnp_1 PBECR4 ? DDE_Tnp_1 DDE_Tnp_Tn3 DUF4158 Resolvase HTH_7 HTH_18 GyrI-like Resolvase HTH_7 ?

WP_225305923.1
NZ_CP044230.1:365376-379735
Streptococcus sp. LPB0220

RNA_helicase Rep_OBD ? ? ? ? EcoRI_methylase GmrSD_N HNH PBECR4 TMEM175 ? Ion_trans_2 DUF389 CsbD Rhomboid VanZ

WP_262751875.1
NZ_JAOPTJ010000038.1:127-9464
Bacillus wiedmannii

HTH_3 MerR_1 Abi_C AbiJ_NTD4 HTH_3 HTH_36 PBECR4 Mob_Pre HTH_Crp_2 HTH_3

WP_238710111.1
NZ_JBQHHY010000001.1:264834-272342
Streptococcus suis

HTH_5 Phage_integrase HTH_17 REP_ORF2-G2P ? ? ? PBECR4 Phage_integrase

WP_144015712.1
NZ_VJXW01000003.1:124859-136705
Criibacterium bergeronii

DUF5699 DUF6017 DUF3801 DUF6877 ? ? ? PBECR4 SAF RcpC ParA-Soj-NTPase T2SSE DUF2678 COX16 ? DUF4320

WP_162163600.1
NZ_JAVLJC010000001.1:214930-227722
Staphylococcus epidermidis

? Encapsidation_CP3 ? ? Terminase_2 DJ-1_PfpI SpoIIM PBECR4 ? SHP Transgly_assoc LysE His_Phos_1 ? Pyr_redox_2 Thioredoxin_3

WP_098158466.1
NZ_NUDH01000050.1:105-6095
Bacillus toyonensis

? HTH_36 ? ? ? ? DUF3967 PBECR4 Resolvase Pox_H7

WP_073460976.1
NZ_CAKMCF010000010.1:115-11891
Enterococcus faecium

EIID-AGA EII-Sor PTSIIB_sorb EIIA-man PTSIIB_sorb PRD EIIA-man PRD NtrC-AAA EutK_C DUF4428 bPH_3 SHOCT DUF5960 PBECR4 Amidase_2 Phage_holin_Dp1 ATG17_like Phage_XkdX

WP_016631725.1
NZ_KE352430.1:58399-70118
Enterococcus faecium LA4B-2

? ? ? ? CSD ? Sigma70_r4 PBECR4 Glyco_hydro_1 PTS_IIB PTS_IIA PTS_EIIC Acetyltransf_7 YrhK ADH_zinc_N_2 ADH_zinc_N ADH_N

WP_096741211.1
NZ_CP023514.1:7778-23202
Enterococcus sp. FDAARGOS_375

FKBP15 PTS_EIIC YdjC GntR UTRA ? Cupin_2 UPF0014 PBECR4 DDE_Tnp_IS240 DUF1541 DUF1541 ? His-Kinase His-Kinase Trans_reg_C Receiver Cu-oxidase_2 Cu-oxidase Cu-oxidase_3 HMA

WP_267165165.1
NZ_JAPMIC010000020.1:16847-36014
Lactococcus lactis

? GTP_EFTU_D3 ? WYL Zn_ribbon_3 Ndc1_Nup YdeJ ZnR Zn_Ribbon_1 DUF805 PBECR4 ? Noelin-1 DUF2130 ABC-ATPase dTDP_sugar_isom ApbA ApbA_C PTS_EIIC_2

WP_263716733.1
NZ_JAOWQM010000009.1:11097-29745
Enterococcus faecalis

RHH_1 MobL ? Eco57I WH_1 DUF8437 Helicase_dom Helicase_C ? SSB SNase PBECR4 AbiH ? ? AAA_14 PHP Resolvase HTH_7 ? DUF530

WP_070873251.1
NZ_JAHLNS010000001.1:1255008-1268917
Staphylococcus caprae

Arg_tRNA_synt_N tRNA-synt_1d DALR_1 HhH-GPD MerR_1 TipAS DUF805 DUF805 Peripla_BP_2 FecCD PBECR4 HAD_2 Abhydrolase_1 SA0570 ? Abhydrolase_1 Staph_reg_Sar_Rot YknX_C Beta-barrel_YknX BSH_YknX

WP_145464179.1
NZ_VELW01000003.1:299084-318059
Staphylococcus hominis

? ? HTH_23 HTH_26 HTH_3 ? Phage_int_SAM_1 Phage_integrase PBECR4 FIVAR FIVAR Rib aRib YSIRK_signal Acetyltransf_7 DUF2871 DUF1775 CopD CopC TetR_N TetR_C_8 CorA

WP_239414238.1
NZ_JAKREP010000001.1:1375-17342
Salinicoccus roseus

Encapsidation_CP3 CHD5 ? ? Peptidase_S78 NUDIX YolD PBECR4 Y1_Tnp NOMO1-like_2nd Ammonium_transp PTS_EIIB PTS_EIIC Alpha-amylase GntR UTRA DNA_pol3_delta2 DNAX_ATPase_lid DNA_pol3_gamma3 DnaX_C

WP_103364316.1
NZ_LR134264.1:1654311-1669186
Staphylococcus simulans

GMIP-like_FCH Phage_YomQ_N Lin0124_C Phage_XkdX DUF7144 TMP_4 Phage_holin_1 CHAP Amidase_2 SH3_5 PBECR4 TM-like_Thioredoxin-like_C GSHPx GTP-bdg_N GTP-bdg_M MMR_HSR1 Met_gamma_lyase ? Gln-synt_C Gln-synt_N MerR_1 PLDc_N HKD HKD

WP_135023458.1
NZ_JADGMC010000002.1:37253-47044
Staphylococcus arlettae

? DUF4763 ? Terminase_4 Encapsidation_CP3 ? ? PBECR4 ? ? LYRIC Glyoxalase Acetylase Adenyl_transf ?

WP_002587148.1
NZ_CP050964.1:2793463-2806065
Enterocloster clostridioformis

TrmB HTH_3 ? HTH_36 T4SS-DNA_transf Toprim_2 DUF3991 Sel1 Sel1 Sel1 Sel1 Sel1 Sel1 Sel1 Sel1 Sel1 MobL PBECR4 DUF6664 RHH_1 DUF6103 DUF6329 NLPC_P60 HTH_3 GGACT

WP_002599778.1
NZ_KB850961.1:964-9979
Clostridium thermobutyricum

NikA-like ? ? Resolvase PBECR4 UFL1 ? ? SH3_3 Holin_BhlA ? SH3_3 SH3_3 SH3_3 SH3_3

WP_025532167.1
NZ_CACRUH010000023.1:28307-45248
Hungatella hathewayi

DUF3100 LysR_substrate HTH_1 malic Malic_M Lar_N LarA_C Fer4_21 Flavodoxin_5 HTH_18 AraC_binding Glyco_hydro_88 PBECR4 HTH_18 Receiver His-Kinase His_kinase HAMP GFO_IDH_MocA_C GFO_IDH_MocA GFO_IDH_MocA GFO_IDH_MocA_C GFO_IDH_MocA BPD_transp_1 BPD_transp_1

WP_242353383.1
NZ_CAKOCO010000004.1:100180-118054
Hungatella effluvii

Glycos_transf_2 MpPF26 dTDP_sugar_isom ABC2_membrane ABC_tran Wzt_C Methyltransf_25 Glycos_transf_2 Glyco_trans_2_3 Glyco_trans_1_4 PBECR4 PDDEXK_9 AAA-ATPase_like NTP_transferase GHMP_kinases_N GHMP_kinases_C Hydrolase_6 Hydrolase_like SIS_2 SIS_2 ? ?

WP_148549601.1
NZ_CYZE01000002.1:359175-377179
Hungatella hathewayi

HATPase_c_5 ZnR dTDP_sugar_isom ABC2_membrane ABC_tran Wzt_C Methyltransf_25 Glycos_transf_2 Glyco_trans_2_3 Glyco_trans_1_4 PBECR4 PDDEXK_9 AAA-ATPase_like NTP_transferase GHMP_kinases_N GHMP_kinases_C Hydrolase_6 Hydrolase_like SIS_2 SIS_2 ? ?

WP_287404572.1
NZ_JAFNSC010000201.1:1-7560
Treponema sp.

? PBECR4 MCPsignal Dynamin_N DUF697 HNH ? ? ?

WP_002706745.1
NZ_AGRW01000055.1:158998-181032
Treponema saccharophilum DSM 2985

LpoB fn3 fn3 fn3 UxaC adh_short_C2 AlaDh_PNT_N AlaDh_PNT_C PNTB_4TM PNTB PBECR4 CoiA_N CoiA_nuc UvrD-helicase UvrD_C ABC_tran ABC_membrane ABC_tran ABC_membrane DUF1302 TP_0789-like MMPL MMPL LCM

WP_172023323.1
NZ_CP116604.1:1068244-1083883
Streptococcus sp. HN38

GntR UTRA UPF0122 SRP54_N SRP54 SRP_SPB SatD Acetylase ABC-ATPase ? PBECR4 ? DUF4322 Abi_2 Abi_2 HTH_3 CRWN_N CRWN_N Gram_pos_anchor Zn_Ribbon_1 ZnR

WP_116485574.1
NZ_QDAF01000012.1:3308-16489
Clostridium perfringens

? ? RHH_1 Terminase_4 ? ? Peptidase_S78 PBECR4 ? Resolvase Recombinase CarD_TRCF_RID CarD_C MS_channel_2nd MS_channel_3rd CutC DUF1269 DUF1576 DUF1576

WP_270373004.1
NZ_JAQDLY010000041.1:16203-24480
Thomasclavelia ramosa

PBECR4 NADH_4Fe-4S Phage_integrase Glyco_hydro_4 Glyco_hydro_4C rve_2 AgrB HATPase_c_5 LytTR Receiver FCD GntR

WP_257069827.1
NZ_JANIKR010000021.1:1-8107
Pediococcus pentosaceus

PhdYeFM_antitox YafQ_toxin PBECR4 HTH_3 RVT_1 DUF536 Rep3_C Rep3_N ? Phage_integrase

WP_061871248.1
NZ_JAXDEG010000001.1:122881-138674
Lactiplantibacillus plantarum

Terminase_4 TerL_ATPase TerL_nuclease DUF7649 Phage_portal Peptidase_S78 Phage_capsid Phage_connect_1 DUF1492 PBECR4 Receiver Trans_reg_C Cache_WalK HAMP PAS His-Kinase His-Kinase YycH YycI Lactamase_B_2 Trypsin PDZ_2 SPOUT_MTase

WP_322192042.1
NZ_CP139637.1:1744635-1755378
Limosilactobacillus fermentum

? Phage_pRha HTH_3 HTH_3 ? DUF6414 ? PBECR4 Arm-DNA-bind_4 Phage_int_SAM_5 Phage_integrase ? CLP_protease TENA_THI-4 HTH_WhiA LAGLIDADG_WhiA WhiA_N CofD PapZ_C RapZ-like_N

WP_139028103.1
NZ_GL538353.1:496481-504700
Listeria grayi DSM 20601

? HTH_Tnp_ISL3 Peptidase_S74 ? DUF1664 Phage_holin_1 Glyco_hydro_25 LysM PBECR4 ? ? ? ? ? ? AA_permease_2

WP_285087299.1
NZ_JASOZK010000001.1:50439-63879
Gemella morbillorum

HTH_19 ? ? ? AAA_25 ? NDNF PBECR4 Receiver Trans_reg_C HAMP His-Kinase His-Kinase PepSY ? ? UPRTase ATP-synt_A

WP_270364323.1
NZ_JAQDQC010000003.1:1293-13771
Enterococcus malodoratus

Ribosomal_L35p Ribosomal_L20 Phage_integrase Phage_int_SAM_3 Arm-DNA-bind_4 ? ? ? Phage_integrase PBECR4 Frataxin_Cyay Resolvase Sigma70_r4_2 ? ? ? ? ?

WP_227100145.1
NZ_JAJJOX010000005.1:217143-229438
Hominenteromicrobium mulieris

ABC_tran ABC_membrane AAA_13 ABC_tran ABC_tran CbiQ Trep_Strep HTH_18 HTH_3 Relaxase PBECR4 ? DUF1016_N Fic-like_C ? AbiEii AbiEi_3_N DUF5699

WP_005341475.1
NZ_CABHNI010000037.1:2917-24842
Dorea formicigenerans

His-Kinase His-Kinase Receiver Glyco_hydro_3_C Fn3-like Glyco_hydro_3 Receiver LytTR HATPase_c_5 Glyco_hydro_3_C Fn3-like Glyco_hydro_3 Glyco_hydro_3 Glyco_hydro_3_C Fn3-like GtrA_DPMS_TM PBECR4 AMP-binding AMP-binding ? PfkB HATPase_c_5 LytTR Receiver Receiver ?

WP_226968597.1
NZ_CAXSLU010000004.1:133839-152389
[Ruminococcus] lactaris CC59_002D

Gate DUF885 Gate JetA DUF4194 AAA_29 SMC_hinge SbcC_Walker_B JetD_C PBECR4 Metallophos_2 NYN OST-HTH OST-HTH ? Eco57I FakA-like_M MarR DUF6198 Cytidylate_kin2

WP_033573172.1
NZ_AYTP01000020.1:386-12991
Lacticaseibacillus rhamnosus L35

ABM Endonuclea_NS_2 ArfC Glyco_trans_1_4 WsaF_N GFO_IDH_MocA YceM-like_C dCMP_cyt_deam_1 ? PBECR4 ? MFS_1 Peptidase_C69 ? ?

WP_270466580.1
NZ_JAQDAI010000008.1:162399-175598
Fusobacterium polymorphum

? FecR_C CarbopepD_reg_2 Secretin_N Secretin AAA-ATPase_like PDDEXK_9 PepSY PepSY DUF1275 ? FTHFS PBECR4 ABC_sub_bind BPD_transp_2 ABC_tran

WP_320950524.1
NZ_CP077181.1:40338-61856
Fusobacterium animalis

? ? OmpA BigA_3rd Autotransporter DUF1275 ? FTHFS PBECR4 Pyridox_ox_2 ParE_toxin DUF6290 ? Transgly_assoc DUF7737 DUF4132 DUF5724 ?

WP_008803204.1
NZ_CP056001.1:1616113-1636682
Fusobacterium animalis

? Toprim Topoisom_bac Toprim_Crpt TnpV WH_1 DUF8437 Helicase_dom Helicase_C ? ? RadC DUF4116 DUF4116 DUF4116 PBECR4 ArdA ? ? Zn_ribbon_DnaG Toprim_2 BetaGal_ABD_1 MobA_MobL ?

WP_243125048.1
NZ_CABHNO010000023.1:81401-97633
Faecalibacterium prausnitzii

? DUF3592 Receiver Trans_reg_C His-Kinase His-Kinase ABC_tran MacB_PCD FtsX MacB_PCD FtsX DUF6061 PBECR4 DUF8370 ABC-ATPase ABC-ATPase DUF6061 DUF2179 Y1_Tnp Ribonuc_L-PSP TctA

WP_009006024.1
NZ_GL988014.1:98383-110899
Fusobacterium necrophorum D12

MobA_MobL ? ? ? DUF4116 MORN_2 EF_HAND_2_PLCG PBECR4 DUF4116 ArdcN VirB8 CagX TrbI ? T4SS-DNA_transf ?

WP_118429708.1
NZ_CATNWV010000005.1:83206-96958
Clostridium perfringens

? DUF6364 RHH_1 Terminase_4 ? ? Peptidase_S78 PBECR4 ? Resolvase Recombinase Zn_ribbon_recom MFS_1 MFS_1 GTP_EFTU EF-G_D2 EFG_III EFG_IV EFG_C ? YcxB SASA

WP_311431786.1
NZ_CAUPDI010000007.1:20286-36400
Facklamia hominis

Gp58 Gp58 ? ? CD1375-like ? Phage_holin_5_1 Glucosaminidase CHAP CW_7 PBECR4 ? CBM_48 Alpha-amylase Alpha-amylase Alpha-amylase_C NTP_transferase Hexapep_GlmU NTP_transferase Hexapep_GlmU Glyco_transf_5 Glycos_transf_1 Transgly Transpeptidase Calcineurin

WP_251852128.1
NZ_CAXYWJ010000044.1:5458-14910
Enterococcus italicus

? DUF2292 ? ? Mb1296_C ? ? PBECR4 ? ? Lactonase AI-2E_transport Ribosomal_S15 RNase_PH RNase_PH_C PNPase RNase_PH RNase_PH_C

WP_266185593.1
NZ_CP111077.1:3593891-3614825
Clostridium sp. LQ25

Tn7_TnsA-like_N Tn7_Tnp_TnsA_C TnsB_N HTH_TnsB Mu-transpos_C AAA_22 TniQ TnsD TnsD DDE_Tnp_IS1595 RrnaAD GTP-bdg_N GTP-bdg_M MMR_HSR1 MMR_HSR1_Xtn PBECR4 DUF6556 TPRs Sirtuin Sirtuin DUF4268 HTH_17 DUF6431 HTH_32 rve rve_3 Mu-transpos_C_2

WP_007893015.1
NZ_AENS01000018.1:147899-166718
Streptococcus pseudoporcinus SPIN 20026

Esterase Peptidase_M10 ABC_tran ABC_tran_Xtn ABC_tran ABC_tran_CTD E1_dh Transket_pyr Transketolase_C Biotin_lipoyl E3_binding E3_binding 2-oxoacid_dh Biotin_lipoyl Pyr_redox_2 Pyr_redox_dim PBECR4 LplA-B_cat Lip_prot_lig_C HTH_18 Collagen Collagen Collagen CFSR Collagen Gram_pos_anchor GATase_3 MurT_C Mur_ligase_M CdaA_N DAC YbbR YbbR YbbR

WP_173750803.1
NZ_JAAIQT010000003.1:39894-56622
Anaerostipes hadrus

Acyl_transf_3 SprT-like Astro_capsid_p NTP_transferase ? Sirtuin nSTAND_NTPase5 HTH_Tnp_1 DUF4160 PBECR4 ABC-ATPase ? ? DUF2677 adh_short_C2 NTP_transferase LpdD_chaperone

WP_008405956.1
NZ_AMCK01000008.1:131895-147083
Solibacillus isronensis B3W22

GATase_6 SIS SIS ? Tn7_TnsA-like_N HTH_3 TniQ TnsD ? AAA_2 PBECR4 FtsX ABC_tran Zip APH ? Methyltransf_25 ?

WP_008701734.1
NZ_AKBT01000001.1:2122625-2136884
Fusobacterium animalis 7_1

? ? ? MobA_MobL ? ? RadC DUF4116 DUF4116 DUF4116 PBECR4 MORN_2 ? ? Zn_ribbon_DnaG Toprim_2 WHD_CvfB ? ? ?

WP_020975286.1
NC_022196.1:1690057-1707489
Fusobacterium vincentii 3_1_36A2

Peptidase_S26 ? ? MuF_C Toprim Topoisom_bac ? ? PBECR4 Zn_ribbon_DnaG DNAG_N Toprim_2 TnpV ? ? ? ? ? ?

WP_023040403.1
NZ_CP159326.1:1559331-1577751
Fusobacterium animalis

T4SS_Ceg9 Peptidase_S26 ? ? Toprim Topoisom_bac ? ? PBECR4 Zn_ribbon_DnaG Toprim_2 TnpV WH_1 DUF8437 Helicase_dom Helicase_C ? ? Epsilon_antitox Zeta_toxin Fic

WP_293842507.1
NZ_CAKPQJ010000010.1:15040-35805
uncultured Phascolarctobacterium sp.

MerR-DNA-bind MerR_1 Ribosomal_S20p SIS SIS GATase_6 GDP_Man_Dehyd Autotransporter HTH_3 Autotransporter PBECR4 Na_Ala_symp Receiver His-Kinase His-Kinase SBP_bac_3 Hpt HD_5 Receiver GGDEF Cob_adeno_trans NDK

WP_304225314.1
NZ_CATZZF010000003.1:12088-29271
Phascolarctobacterium succinatutens

Met_synt_B12 S-methyl_trans Pterin_bind B12-binding_2 B12-binding ? LrgB LrgA Clp_N AAA AAA_lid_9 AAA_2 ClpB_D2-small ? PBECR4 AIRC GATase_7 Pribosyltran AIRS AIRS_C Formyl_trans_N MGS AICARFT_IMPCHas GARS_N GARS_A GARS_C IMPDH

WP_056961633.1
NZ_AYZI01000004.1:105083-116921
Fructilactobacillus florum DSM 22689 = JCM 16035

LapA_dom DHH DHHA1 RecJ_OB ssDNA-exonuc_C Pribosyltran DUF7420 ? DUF1492 ? PBECR4 ? HNH Terminase_4 ? PA_decarbox ? Glyco_transf_8

WP_196032844.1
NZ_JADPFI010000167.1:39631-47243
Flavonifractor plautii

? Phage-tail_3 ? Phage_lysozyme2 Amidase_2 Sbt_1 ? ? PBECR4 dsrm Ribonucleas_3_3 PP-binding FA_synthesis

WP_019380419.1
NZ_CP015506.1:4113451-4126013
Cytobacillus oceanisediminis 2691

Methyltransf_28 DUF2626 MetOD1 HTH_20 ArsC YozF ? TetR_C_39 PBECR4 ? DUF3885 TIR Zn_peptidase_2 SduA_C ? ?

WP_318060969.1
NZ_JAWPEO010000016.1:12603-27623
Bacillus infantis

SpoVAC_SpoVAEB SpoVAD SpoVAC_SpoVAEB Spore_YhcN_YlaJ DUF1657 ? MPTase-PolyVal ArdcN PBECR4 ? Spore_GerAC Spore_GerAC_N GerA Spore_permease DDE_Tnp_1 GyrI-like HTH_18 HTH_7 Resolvase

WP_116354735.1
NZ_JBBPAM010000002.1:2353-16105
Fredinandcohnia sp. FSL W7-1320

Rep3_C Rep3_N EzrA rve_2 rve HTH_21 HTH_Tnp_1 ? ? ParA-Soj-NTPase RH3_dom PBECR4 Peptidase_S8 Fervidolysin_NPro-like ? Coat_F Coat_F DUF1657 Spore_YhcN_YlaJ SpoVAC_SpoVAEB

WP_314428123.1
NZ_CAUSCP010000053.1:150-5263
Leuconostoc lactis

Glyco_hydro_25 Phage_holin_6_1 PBECR4 ? Guanylate_kin RNA_pol_Rpb6 Pro_isomerase S1 ?

WP_039143230.1
NZ_JOJZ01000009.1:49829-68892
Fructilactobacillus fructivorans

DUF421 YetF_N DUF3290 DUF4079 DUF4181 ? ADH_zinc_N_2 ADH_N DNA_binding_1 ? PBECR4 Cas_Cas1 CRISPR_Cas2 Cas_Csn2 ? MacP_activator FGGY_N FGGY_C ApbA ApbA_C

WP_147657293.1
NZ_CP042371.1:1221643-1234368
Secundilactobacillus malefermentans

? HTH_3 ? HTH_28 DEDD_Tnp_IS110 Transposase_20 ? HTH_1 LysR_substrate PBECR4 LysR_substrate HTH_1 Oxidored_FMN HTH_19 ? SIS PemK_toxin RelB

WP_221679503.1
NZ_JAASHU010000032.1:45583-52112
Enterococcus sp. K18_3

DUF1642 N6_N4_Mtase DNA_methylase HTH_3 PBECR4 ? ? Methyltransf_25 DNA_methylase Phage_VG64 MazG ?

WP_052177913.1
NZ_JAKVDS010000006.1:40670-55399
Staphylococcus haemolyticus

? HTH_23 HTH_26 HTH_3 ? DUF8426 Phage_integrase PBECR4 GMP_synt_C tRNA_Me_trans GATase IMPDH Xan_ur_permease Pribosyltran YflT ? SDF

WP_101033496.1
NZ_CP079950.1:686324-703179
Macrococcoides caseolyticum

? ? NAGPA YomR_C TT1_Tal Prophage_tail Peptidase_S74 DUF7365 Holin_SPP1 Amidase_2 SH3b_T PBECR4 CorA UPF0014 ABC_tran DUF72 TauE Calcineurin 5_nucleotid_C LIAS_N Radical_SAM

WP_062806602.1
NZ_JAKEJU010000001.1:629142-645386
Streptococcus uberis

Sipho_tail SPP1_Dit ? ? CENP-F_leu_zip Phage_holin_1 Amidase_2 ? PBECR4 DUF5960 VTT_dom ABC2_membrane_4 ABC_tran GntR PHP DNA_pol3_alpha DNA_pol3_finger HHH_6 N-OB PFK

WP_012738486.1
NC_012778.1:234601-249915
Lachnospira eligens ATCC 27750

Bro-N FRG ? HTH_3 Peptidase_M78 FMN_red Gp49 HTH_3 PBECR4 HTH_3 ? ? pEK499_p136 LMWPc Acetylase MreB_Mbl

WP_308802644.1
NZ_WGXE01000001.1:1188-19880
Agathobacter sp.

Phage_integrase Phage_int_SAM_1 Phage_integrase Phage_integrase Toprim Topoisom_bac Toprim_Crpt Toprim_Crpt Toprim_Crpt Toprim_Crpt Toprim_Crpt GMPPB_C Hexapep NifU_N GGGtGRT PBECR4 SdpI Peptidase_C39_2 Receiver Trans_reg_C HAMP His-Kinase His-Kinase ? Glyco_hydro_2_N Glyco_hydro_2 Glyco_hydro_2_C Bgal_small_N

WP_064608987.1
NZ_LXKF01000011.1:39800-50810
Streptobacillus moniliformis

? TrbL Peptidase_S26 TraD TSP3_bac ? DUF4116 DUF4116 PBECR4 YadA_anchor OmpA DUF4116 DUF4116 DUF4116 NLPC_P60 DUF3991 Toprim_2 DUF4116 DUF4116 DUF4116 DUF4116 DUF4116 PBECR4

WP_172611249.1
NZ_LR215983.1:4009968-4029801
Eubacterium limosum

Sigma70_r4_2 Sigma70_r2 Flg_new Flg_new Flg_new Flg_new ADH_N ADH_zinc_N HTH_3 DUF739 ? ? PBECR4 Peptidase_S8 Peptidase_S8 Cyclophil_like2 FMN_red Hexapep_2 Hexapep HTH_1 LysR_substrate TauE DUF1659

WP_207179914.1
NZ_AP024480.1:2464800-2481089
Anaerocellum diazotrophicum

Thioredoxin_3 ArsP_1 HTH_5 ? Peptidase_M48 Peptidase_M48 ? ? PBECR4 HTH_3 Peptidase_M78 DUF3368 CTXL_M ? ? ? Transposase_31 HTH_Rpn_C

WP_288304446.1
NZ_CAJMBC010000039.1:1111-17370
uncultured Treponema sp.

DUF6788 AAA_14 Hydrolase_3 PGM_PMM_III PGM_PMM_I tRNA-synt_1f Anticodon_2 ? Sm_multidrug_ex PTA_PTB PBECR4 HSDR_N_2 Aminotran_4 MatE MatE MethyltransfD12 LRRs Flg_new

WP_013712114.1
NC_015392.1:1-7061
Salmonella enterica subsp. enterica serovar Dublin

? PBECR4 MerR_1 DUF3967 Mob_Pre ? Rep_1 TPRs RapH_N TPRs RapH_N

WP_253210185.1
NZ_JACACB010000023.1:1359-12771
Tetragenococcus halophilus

? ? BppU_N ? PUMA_CC Phage_holin_5_2 Amidase_2 SH3_5 PG_binding_1 PBECR4 His_Phos_1 OB_YrrC HHH_RecD2 AAA_19 SH3_13 UvrD_C_2 QueT ? DAGK_cat YegS_C CBS Ribosomal_L33

WP_014124444.1
NC_016052.1:1038883-1053132
Tetragenococcus halophilus NBRC 12172

? Receiver Trans_reg_C His-Kinase ABC_tran FtsX FtsX ? SAP PBECR4 ECF_trnsprt ABC_tran ABC_tran CbiQ Receiver LytTR HTH_3 Zn_ribbon_2 DUF1706

WP_014279454.1
NC_016641.1:2120515-2138255
Paenibacillus terrae HPL-003

Polysacc_deac_1 Malt_amylase_C Alpha-amylase ? adh_short Str_synth SSL_N ADH_zinc_N ADH_N EAL PBECR4 5_nucleotid_C Calcineurin PNPOx_N NMT1 Thiamine_BP BPD_transp_1 ABC_tran TatD_DNase

WP_214525665.1
NZ_CAJETT010000001.1:462296-476328
Staphylococcus pseudintermedius

? ? Lipase_GDSL_2 BppU_N FAM81B BppU_N Lipase_GDSL_2 Phage_holin_4_1 Amidase_2 SH3b_P2 PBECR4 ? Hol_Tox Phage_Mu_F ? DUF4355 Leukocidin Leukocidin

WP_241519976.1
NZ_MWRM01000010.1:12259-26156
Staphylococcus delphini

GCV_H Toprim Thioredoxin ABC_tran NIL BPD_transp_1 Lipoprotein_9 Lipoprotein_9 PBECR4 VCA0040-like ABC_tran SufBD_N SUFBD_core Aminotran_5 NifU_N SufBD_N SUFBD_core DJ-1_PfpI

WP_270289742.1
NZ_JALKPN010000001.1:586805-600911
Enterococcus casseliflavus

D5_N DUF5906 Pox_D5 DUF3206 ? DUF2292 ? ? ? PBECR4 ? ? ? ABC_tran HTH_3 Trep_Strep CbiQ

WP_016991690.1
NZ_AJXM01000013.1:361-8857
Lysinibacillus boronitolerans F1182

HTH_26 ? ? ? PBECR4 Resolvase HTH_7 ? ? ? Bro-N ANT ? DUF6912

WP_276359971.1
NZ_JARKHZ010000005.1:379335-389678
Bacillus amyloliquefaciens

? ? HIT Abhydrolase_1 ? EndoU_bacteria YolD PBECR4 HTH_17 LXG CdiI_ImmP CdiI_2

WP_019244574.1
NZ_CAPG01000097.1:11988-16629
Bacillus sp. AP8

PBECR4 ? ? ? HTH_Tnp_1_2 ? ? CdvB_HTH

WP_019637870.1
NZ_KB907256.1:166262-176103
Paenibacillus fonticola DSM 21315

HTH_26 HTH_3 PBECR4 Flavodoxin_2 MarR_2 tRNA_bind NMT1_2 HTH_17 FAD_binding_2 Succ_DH_flav_C Fer4_7 Phosphonate-bd NMT1

WP_019893241.1
NZ_KB913034.1:1320701-1336627
Allobaculum stercoricanis DSM 13633

HTH_Crp_2 NtrC-AAA PRD EIIA-man PRD MatE MatE MarR_2 PFK BPD_transp_1 Glycos_transf_2 SRP54_N SRP54 SRP_SPB PBECR4 Ribosomal_S16 KH_KhpA-B RimM PRC_RimM tRNA_m1G_MT Peptidase_M15_4 Ribosomal_L19 Peptidase_S26

WP_251469489.1
NZ_JAMATK010000001.1:371083-382573
Staphylococcus equorum

DUF4763 ? Terminase_4 Encapsidation_CP3 ? ? ? PBECR4 ? ? Acetyltransf_7 HAD_2 Acetylase Glyoxalase Acetylase

WP_195948409.1
NZ_JADPGU010000045.1:132-13220
Paraclostridium bifermentans

? CTD6 MC2 AAA_23 TSC22 Resolvase ? ? PBECR4 ? HNH Mor ? YvrJ

WP_128630829.1
NZ_JAZHPZ010000014.1:471-13069
Paenibacillus haidiansis

PLDc_N HKD HKD DUF1805 DpaA_N 2-Hacid_dh_C Phage_integrase FBA_1 ? ? PBECR4 Phage_integrase DUF2642 DUF1657 PG_binding_1 YkuD Hydrolase_2 ? Polysacc_deac_1

WP_021869492.1
NZ_QUCM01000002.1:234849-251614
Clostridium sp. AM22-11AC

Polysacc_deac_1 RuvB_N AAA_assoc_2 MgsA_C Rho_N Rho_RNA_bind ATP-synt_ab PGM_PMM_I PGM_PMM_II PGM_PMM_III PGM_PMM_IV ABC_trans_CmpB Phage_integrase Phage_integrase Phage_int_SAM_4 PBECR4 MreB_Mbl OB_YrrC HHH_5 HHH_RecD2 AAA_19 SH3_13 UvrD_C_2 DZR_2 Pribosyltran Ribosomal_L33 SecE NusG KOW Ribosomal_L11_N Ribosomal_L11

WP_262579332.1
NZ_JAOQJM010000002.1:491642-501745
Blautia acetigignens

? Terminase_4 PBECR4 DDE_Tnp_1_3 Peptidase_S26 DUF6783 DUF6783 GATase_7 Asn_synthase ABC_tran FtsX MacB_PCD FtsX

WP_195275677.1
NZ_JADNAB010000018.1:35382-51132
Roseburia faecis

ABC_tran BPD_transp_1 NMT1 Com_YlbF Sulfatase SGSH_C Radical_SAM SPASM LacI Peripla_BP_3 AAA-ATPase_like PDDEXK_9 PBECR4 HhH-GPD ? Acetylase ? AAA_14 DUF4143 HipA_C Peptidase_C39_2

WP_293615232.1
NZ_FR898094.1:73400-93687
Ruminococcus sp. CAG:330

CHASE9 CBM_35 Glyco_hydro_26 ? ? MuF_C DUF4407 DUF4316 ? Zn_ribbon_DnaG DUF3991 Toprim_2 Eco57I WH_1 DUF8437 Helicase_dom Helicase_C PBECR4 ? TnpV RIFIN TraX ETC_C1_NDUFA5 ? HTH_ParB ParB_N

WP_027215576.1
NZ_AUKD01000004.1:48386-64191
Butyrivibrio fibrisolvens MD2001

Peptidase_Prp Ribosomal_L21p Glycos_transf_2 GGDEF RNase_E_G RNase_E_G DUF2344 Radical_SAM Radical_SAM_N2 PBECR4 Zn_Ribbon_1 ABC_tran ? GYF Band_7_1 ZnR PRA-PH PRA-CH His_biosynth IGPD

WP_074756385.1
NZ_FOGJ01000013.1:73243-89759
Butyrivibrio fibrisolvens

BPD_transp_1 BPD_transp_1_N SBP_bac_5 Methyltrans_SAM PUA_3 Zn_ribbon_NUD NUDIX HTH_3 ? Sigma70_r4_2 Sigma70_r2 PBECR4 Sigma70_r4_2 ? MerR_1 Baculo_PEP_C Spectrin_2 Acetylase ? Hydrolase_4 Abhydrolase_4 ?

WP_023049743.1
NZ_KI518218.1:1-6166
Cetobacterium somerae ATCC BAA-474

Rep3_C Rep3_N PBECR4 ? ? Relaxase MobC NikA-like ? ? SEC-C

WP_063602536.1
NZ_LITQ01000050.1:1-15937
Clostridium coskatii

Methylase_S Methylase_S SLFN_AlbA_2 HATPase_c_4 Sigma70_r2 Sigma70_r4 YvrJ DUF1659 DUF2922 Amidase_2 PG_binding_1 PBECR4 SLFN_AlbA_2 YobI-ATPase ? DDE_Tnp_IS66_C DDE_Tnp_IS66 zf-IS66 LZ_Tnp_IS66 TnpB_IS66

WP_023355293.1
NZ_KI535369.1:170885-193818
Catonella morbi ATCC 51271

? SSB NLPC_P60 HTH_17 ? DUF8193 DUF8194 DUF8195 ? PBECR4 ? ? TraC-like P-loop_TraG ? UPF0236 Radical_SAM

WP_323679133.1
NZ_JAVMJT010000001.1:488860-503477
Exiguobacterium indicum

Peptidase_M3_N Peptidase_M3 DeoRC Rib_5-P_isom_A ? ? ? ? YolD PBECR4 DUF350 ? GGDEF 5TM-5TMR_LYT GntP_permease CoA_trans CoA_trans adh_short

WP_099778118.1
NZ_ASBQ01000006.1:51352-63883
Streptococcus suis YS107

Gram_pos_anchor 5_nucleotid_C Calcineurin HD_4 RelA_SpoT TGS RelA_AH RelA_RIS ACT_4 Tyr_Deacylase ? Hol_Tox Receiver LytTR HATPase_c_5 PBECR4 ? ? ? ? ? ? RecX_HTH3

WP_025654019.1
NZ_BQNQ01000001.1:170915-187412
Faecalicatena contorta

Peripla_BP_4 BPD_transp_2 GrpB ? ? BPD_transp_1 BPD_transp_1 PBECR4 SBP_bac_8 His-Kinase His_kinase HAMP dCache_1 HTH_18 Receiver DUF1349 PHP Hexapep Mac DeoRC HTH_DeoR

WP_025696052.1
NZ_ASSC01000003.1:1-14232
Paenibacillus forsythiae T98

? Cys_Met_Meta_PP DeoC Band-7 PTS-HPr DAHP_synth_1 CM_2 AA_permease PBECR4 GGDEF Receiver MpsC MpsC Oxidored_nitro Oxidored_nitro

WP_325877059.1
NZ_JAMWKT010000002.1:466044-474050
Mammaliicoccus sciuri

PriCT_1 ? TscT HTH_23 HTH_17 HTH_31 Phage_int_SAM_3 Phage_integrase PBECR4 Ribosomal_S18 SSB Ribosomal_S6 YchF-GTPase_C ? HTH_7 Resolvase ?

WP_026510791.1
NZ_AUJU01000015.1:69848-90068
Butyrivibrio sp. LC3010

Prenyltransf CTP_transf_1 DXP_reductoisom DXP_redisom_C DXPR_C Peptidase_M50 GcpE GcpE_C DNA_pol3_a_NI N-OB RNase_T DNA_pol3_alpha DNA_pol3_alpha DNA_pol3_finger HHH_6 ? PBECR4 FGGY_N FGGY_C ECF_trnsprt RimP_N DUF150_C NusA_N S1 KH_NusA_1st KH_NusA_2nd YlxR Ribosomal_L7Ae IF2_N IF2_N GTP_EFTU EF-G_D2 IF-2 GTP_EFTU_D2

WP_026512276.1
NZ_KE384181.1:4165-24008
Butyrivibrio sp. LC3010

? Flavin_Reduct RUBY_RBDX ? ABC-ATPase DUF3226 ? AAA_18 PBECR4 Big Big Big KilA-N ABC-ATPase RloB Ig_Eae Big LRRs

WP_026667415.1
NZ_JMMD01000007.1:174295-188060
Butyrivibrio sp. AE2005

Zn_ribbon_DnaG ? ? ? PadR ? ? PBECR4 AEP-TOTE ResIII HKD Peptidase_S66 Peptidase_S66C CEP63 ? Orn_Arg_deC_N Orn_DAP_Arg_deC ?

WP_026663480.1
NZ_KK211284.1:95983-113068
Butyrivibrio proteoclasticus FD2007

MecA ? ? ? RrnaAD Zn_ribbon_NUD NUDIX Rce1-like PBECR4 Bro-N Flavin_Reduct HTH_18 AraC_binding ABC_tran ABC_tran BPD_transp_2 ? BPD_transp_2

WP_035796412.1
NZ_JMLK01000043.1:11015-14484
Clostridium akagii DSM 12554

? DUF6768 ? ? ? ? ? ?

WP_026895954.1
NZ_JHVL01000068.1:6-10871
Clostridiisalibacter paucivorans DSM 22131

PBECR4 SLH SLH ? HD_5 YdjM

WP_027400214.1
NZ_KE384518.1:86717-100733
Anaerovorax odorimutans DSM 5092

HTH_OrfB_IS605 OrfB_IS605 Cas12f1-like_TNB IGPD GATase His_biosynth His_biosynth DUF3239 PRA-CH PRA-PH PBECR4 BPL_C BPL_LplA_LipB HTH_11 ? HTH_11 ABC_membrane ABC_tran ABC_membrane ABC_tran Rrf2 ABC_tran NIL

WP_028105294.1
NZ_JHZV01000008.1:88742-103668
Exiguobacterium undae DSM 14481

? ? ? ? ? ? ? PBECR4 Phage_int_SAM_1 Phage_integrase PIN Abi_C AbiJ_NTD4 ? ParA-Soj-NTPase Resolvase ?

WP_235044677.1
NZ_ATKG01000043.1:233-10559
Fusobacterium hwasookii ChDC F300

? RadC DUF4116 DUF4116 DUF4116 PBECR4 MORN_2 ? Zn_ribbon_DnaG Toprim_2 WHD_CvfB ? DUF4238 Epsilon_antitox Zeta_toxin

WP_184094637.1
NZ_AP023367.1:432438-447207
Anaerocolumna cellulosilytica

HTH_3 ? AAA_25 ? CC149 MoxR-AAA DUF2357 PBECR4 PemK_toxin Phage_integrase Phage_int_M HTH_3 HTH_3 ? ? D5_N DUF5906 Pox_D5

WP_125706004.1
NZ_JBHTOO010000003.1:527733-540863
Companilactobacillus mishanensis

? Lebercilin Phage_holin_5_2 Amidase_2 Transgly_assoc ? CsbD PBECR4 Rce1-like ABC_membrane ABC_tran ABC_membrane ABC_tran Beta-lactamase MurT_C Mur_ligase_M TK PCRF RF-1

WP_033169786.1
NZ_JNKI01000008.1:49468-57224
Selenomonas sp. ND2010

PBECR2 DpnI_C DpnI MethyltransfD12 YvrJ DUF2922 DUF1659 ? PBECR4 Amidase_3 HTH_67 ? ? HTH_36 HTH_17 HTH_3

WP_047335118.1
NZ_LDEA01000046.1:1-14018
Enterococcus cecorum

PhageMin_Tail Sipho_tail SPP1_Dit Prophage_tail Collagen BppU-like_C Collagen Collagen Gp58 Peptidase_S74 ? VPA1267 Phage_holin_4_1 Amidase_5 SH3_5 PBECR4 ? Y1_Tnp HTH_OrfB_IS605 OrfB_IS605

WP_051929761.1
NZ_JBSMXV010000028.1:9177-19786
Carnobacterium mobile

? ? DUF3954 ? DUF771 ? ? PBECR4 GidB ParA-Soj-NTPase ParB_N HTH_ParB ParB_C DUF951 MMR_HSR1 YchF-GTPase_C DUF1129 ?

WP_264934799.1
NZ_JAPDOE010000013.1:1649-18859
Paenibacillus sp. LS1

AP_endonuc_2 BetaGal_gal-bd BetaGal_ABD_1 Glyco_hydro_35 Discoidin Alpha_L_fucos CutC BNR_2 BNR_2 ? Glyco_hydro_3 Fn3-like Glyco_hydro_3_C PBECR4 LtrA Glyoxalase Glyoxalase DUF896 Zn_ribbon_3 Band_7_1 TPM_phosphatase Zn_Ribbon_TF PspA

WP_155619263.1
NZ_CP086393.1:908166-920984
Paenibacillus macerans

Phage_TAC_5 DUF2001 Phage_sheath_1C Phage_sheath_1 Phage_sheath_domII YqzN_YkzM Phage_tail_terminator_8 Cu_amine_oxidN1 CCDC-167 PBECR4 AIPR SLFN-g3_helicase MazG-like HIT HTH_3 HTH_3 ?

WP_303725922.1
NZ_SVBT01000013.1:17921-31627
Anaerovibrio lipolyticus

YqfB GtrA_DPMS_TM Glycos_transf_2 DUF4634 ? Med23 Resolvase PBECR4 SSF Receiver CheX CheX DUF1934 Arg_tRNA_synt_N tRNA-synt_1d DALR_1 HARE-HTH CTP_synth_N GATase

WP_208969158.1
NZ_CP040413.1:1701208-1731969
Dolosigranulum pigrum

TnpB_IS66 GA GA GA GA GA GA DUF1542 DUF1542 DUF1542 DUF1542 DUF1542 DUF1542 DUF1542 DUF1542 GA GA GA GA GA GA GA YSIRK_signal GA GA GA GA GA GA YSIRK_signal GA GA YSIRK_signal RF-1 PCRF SecA_SW P-loop_SecA P-loop_SecA SecA_DEAD SLAC1 PBECR4 GRDB ? Aminotran_5 Hydrolase_4 2-oxoacid_dh E3_binding Biotin_lipoyl SelA Se-cys_synth_N WHD_3rd_SelB WHD_2nd_SelB Beta-barrel_SelB GTP_EFTU_D2 GTP_EFTU

WP_119610846.1
NZ_JBSGLX010000001.1:1-12159
Staphylococcus xylosus

SH3_5 PBECR4 PepSY Peptidase_M42 Thioredoxin DUF1444 DUF4479 tRNA_bind FtsK_alpha FtsK_SpoIIIE FtsK_gamma Mur_ligase Mur_ligase_M Mur_ligase_C

WP_069158895.1
NZ_DBFYTC010000232.1:5451-30268
Eisenbergiella tayi

? GntR GntR Ig_mannosidase Mannosidase_ig Glyco_hydro_2 Glyco_hydro_2_N2 DUF6034 DUF6034 His-Kinase His-Kinase HAMP Trans_reg_C Receiver SpoVAC_SpoVAEB PBECR4 HTH_18 Receiver His-Kinase His_kinase SBP_bac_8 Glyco_hydro38C2 Glyco_hydro_38C Alpha-mann_mid Glyco_hydro_38N Glyco_hydro_106 SBP_bac_1 BPD_transp_1

WP_045175477.1
NZ_CP139957.1:2078787-2089696
Anaerocellum danielii

IstB_IS21 Zn_ribbon_RRN7 ? HTH_3 HTH_3 HicB Arc AAA_11 AAA_12 PBECR4 PIN DUF4743 ? ? ? Fic ?

WP_325999123.1
NZ_JALLNK010000001.1:523226-538230
Staphylococcus pseudoxylosus

CHAP Amidase_2 SH3_5 ? ? TauE adh_short DUF3139 Acyl_LnsA PBECR4 MFS_1 HxlR Tautomerase DUF1093 ? ? HTH_26

WP_248559190.1
NZ_CP064868.1:2566283-2581379
Mammaliicoccus sciuri

? TSC22 ? ? ? Phage_holin_1 CHAP Amidase_2 SH3_5 PBECR4 SnoaL_3 YolD ? ZnuA ZinT Methyltransf_31 Peripla_BP_2 DUF7916

WP_214617565.1
NZ_CP190760.1:1-4706
Streptococcus mitis

? ? ? NikA-like ? FtsK_SpoIIIE Rep_trans Rep_trans

WP_050678796.1
NZ_LFQN01000031.1:677-15934
Exiguobacterium acetylicum

GCP_N_terminal ? ? ? ? ? ? PBECR4 ? DDE_Tnp_1_6 Antitox_RHH ParA-Soj-NTPase ? ? ?

WP_242846237.1
NZ_LN868536.1:148768-165680
Anaeromassilibacillus senegalensis

Dockerin_1 FIVAR NPCBM NPCBM NPCBM_assoc Melibiase_C Melibiase_2 Melibiase_2 SfLAP FIVAR FIVAR TackOD1 DUF2461 Bactofilin Bactofilin DUF4004 PBECR4 FakA-like_M ? MazE_antitoxin DUF4428 SIS_2 SIS_2 ROK Peripla_BP_4 BPD_transp_2

WP_050891555.1
NZ_CP020731.1:1599501-1614678
Leuconostoc mesenteroides subsp. mesenteroides

? Prophage_tail ? BppU_N DUF7121 Pect-lyase_RHGA_epim ? Glyco_hydro_25 ? PBECR4 ? ? Hexapep Hexapep Cys_Met_Meta_PP PALP KxYKxGKxW_sig Cthe_2159 rve HTH_38

WP_051258569.1
NZ_AUCD01000127.1:417-1079
Atopococcus tabaci DSM 17538

PBECR4

WP_260252370.1
NZ_RITX01000008.1:246-7414
Levilactobacillus brevis

? ? Phage_XkdX ? ? ? Glyco_hydro_25 DUF5776 DUF5776 PBECR4 ? ? ?

WP_195226536.1
NZ_JADMWF010000006.1:83752-99730
Weissella confusa

Sipho_tail SPP1_Dit Sipho_Gp37 BppU_IgG ? DUF2730 Phage_holin_6_1 Glyco_hydro_25 PBECR4 SHOCT ? Glyco_hydro_3 Glyco_hydro_3_C Fn3-like ? ? ABC_membrane ABC_tran Chorismate_bind

WP_057783003.1
NZ_BJWE01000006.1:48605-61239
Pediococcus parvulus

? HTH_36 DnaB_2 IstB_IS21 PF0610-like_N ? ? ? PBECR4 Hydrolase_4 Abhydrolase_2 DAGK_cat YegS_C DUF915 Aldo_ket_red Thioredoxin MgtC DUF915 DUF915

WP_171030797.1
NZ_VBTH01000012.1:1-8134
Pediococcus stilesii

Amidase_2 PBECR4 Polysacc_synt S4 PseudoU_synth_2 Carb_kinase Usp dNK Hydrolase_3 DUF4229

WP_058002207.1
NZ_VKHZ01000051.1:187-11687
Heyndrickxia oleronia

? Phage_int_SAM_1 Phage_integrase ? ? ? SLH PXO2_28_C PBECR4 HTH_17 Dicers_N DRC10_N ? ? ? HTH_49 Resolvase DUF3951

WP_058591705.1
NZ_LDTK01000057.1:39809-45699
Mammaliicoccus sciuri

? ? CCDC93_CC Phage_holin_1 Peptidase_M23 Amidase_2 SH3b_P2 ? HTH_3 PBECR4 ? YolD ?

WP_060937318.1
NZ_KQ959336.1:117-8003
Aerococcus christensenii

DUF1841 ArdcN Peptidase_M78 PBECR4 ? MobL Zn_ribbon_DnaG DUF3991 Toprim_2 ? RadC Epiregulin_C Sortase Endonuclea_NS_2

WP_061993481.1
NZ_DF968005.1:120488-135616
Fructobacillus ficulneus

TGS tRNA_SAD tRNA-synt_2b HGTP_anticodon AA_permease VTT_dom ? NAMPT_N NAPRTase Fructosamin_kin ECF_trnsprt PBECR4 UPRTase Peptidase_S11 LEA1_2_D7_KIN2 Peptidase_M24 Methyltr_RsmF_N Methyltr_RsmB-F RsmF_methylt_CI Methyltranf_PUA DUF1831 His_Phos_1

WP_063602579.1
NZ_LITQ01000052.1:1596-21171
Clostridium coskatii

? DUF2971 DUF6261 SH3_3 ABC-ATPase ? AAA_15 OLD-like_TOPRIM UvrD-helicase UvrD_C PBECR4 ? CW_binding_2 CW_binding_2 CW_binding_2 HB_LcnD ? DUF4143 ? Transposase_mut

WP_283600939.1
NZ_CANCWS010000002.1:68709-87799
Ligilactobacillus aviarius

Stealth_CR1 Stealth_CR2 Stealth_CR3 Stealth_CR4 EpsG Polysacc_synt Glyco_transf_4 Glycos_transf_1 LytR_cpsA_psr Big Collagen_bind SpaA Gram_pos_anchor YfhO PBECR4 Glyco_hydro_2_N Glyco_hydro_2 Glyco_hydro_2_C Glyco_hydro_2_C Phosphonate-bd ABC_tran BPD_transp_1 BPD_transp_1 Calcineurin 5_nucleotid_C

WP_064592371.1
NZ_LWTI01000058.1:209-3345
Streptobacillus moniliformis

DUF4116 DUF4116 PBECR4 NLPC_P60 DUF3991 Toprim_2

WP_153705208.1
NZ_WJNA01000028.1:1-15506
Limosilactobacillus reuteri

? ? Lreu_0056_like HTH_3 KxYKxGKxW_sig Gram_pos_anchor SocA_Panacea EMP24_GP25L PBECR4 ? Gram_pos_anchor ? DivIC ? Resolvase HTH_28 Resolvase

WP_068471764.1
NZ_CABSDR010000037.1:1-13984
uncultured Parvimonas sp.

DNA_methylase Zn_ribbon_DnaG DUF3991 Toprim_2 WH_1 DUF8437 Helicase_dom Helicase_C PBECR4 ? Relaxase NikA-like DnaJ

WP_068591275.1
NZ_FTNK01000047.1:294-8705
Paenibacillus macquariensis

? HTH_36 ? ? ? Phage_capsid HTH_17 ? NYD-SP28 MerR_1 ?

WP_070616932.1
NZ_KV797910.1:171636-185853
Aerococcus sp. HMSC062A02

? ? ? ? ? Phage_holin_6_1 Glucosaminidase CHAP CW_7 PBECR4 MS_channel_1st_1 MS_channel_1st_1 MS_channel_1st_1 MS_channel_1st_1 CAMP_factor CAMP_factor CAMP_factor PALP Hexapep Hexapep CorA Orn_Arg_deC_N GFO_IDH_MocA DAPDH_C

WP_073590749.1
NZ_FRFD01000013.1:153129-168620
Anaerocolumna xylanovorans DSM 12503

Resolvase HTH_37 ? ? ? ? ? DNA_methylase AAA_15 ABC-ATPase ? Tn916-Xis Integrase_DNA Phage_int_SAM_3 Phage_integrase ? ? Zn_ribbon_8 ? Sigma70_r2 Sigma70_r4_2

WP_256210168.1
NZ_FOLZ01000010.1:17056-27790
Streptococcus gallolyticus

Sipho_tail Prophage_tail CCDC39 CBM_4_9 Gp58 ? ? Phage_holin_4_1 Phage_holin_Dp1 ? PBECR4 Phage_Gp111 AcrIIA6 ?

WP_074889469.1
NZ_FOXO01000020.1:11883-24754
Butyrivibrio proteoclasticus

Acetylase ? ? DUF1186 SEC-C ABC2_membrane_2 HTH_3 ? PBECR4 ? ? ? YitT_membrane DDE_Tnp_1 ? GerE

WP_224383312.1
NZ_CP075986.1:12898-27076
Clostridium perfringens

? ? ? ? ? ? ? ? TIR GP3_package Terminase_3 Terminase_3C SPP1_portal Phage_Mu_F DUF4355 Phage_capsid_4

WP_075818558.1
NZ_CAJUTZ010000039.1:3557-17050
Ileibacterium valens

tRNA_bind B3_4 B5 tRNA_synthFbeta FDX-ACB Antibiotic_NAT TPRs BPD_transp_1 Glycos_transf_2 ? SRP54_N SRP54 SRP_SPB PBECR4 Ribosomal_S16 KH_KhpA-B RimM PRC_RimM tRNA_m1G_MT

WP_076101027.1
NZ_MKQN01000059.1:1814-15077
Paenibacillus odorifer

? ? ? ? ? ? ? PBECR4 PKD_4 ? ? ? MobA_MobL DUF3847 SpoOE-like

WP_249974206.1
NZ_JAFNEF010000013.1:413-8225
Enterococcus faecium

? ? ? ? YopX ? ? PBECR4 FRG ? ? DUF6290 ParE_toxin

WP_311874745.1
NZ_JARQCB010000002.1:457114-470531
Vagococcus carniphilus

PseudoU_synth_1 PseudoU_synth_1 Ribosomal_L13 Ribosomal_S9 Phage_integrase Resolvase ? LysM MucBP PBECR4 ? ? ? ? ? ? ?

WP_087417267.1
NZ_NFHH01000007.1:54057-69297
Blautia sp. An81

Bgal_small_N LacZ_4 Glyco_hydro_2_C Glyco_hydro_2 Glyco_hydro_2_N Flavodoxin_4 ArAE_1_C ArAE_1 ? His-Kinase His-Kinase Trans_reg_C Receiver Rrf2 PBECR4 CsxB VWA ThiW Sigma70_r2 Sigma70_r4_2 DUF4179 DUF5643 HPPK FolB Pterin_bind HD

WP_087572446.1
NZ_MXQD01000074.1:4838-18720
Paenibacillus sp. MY03

ApbE NusG_II Hpre_diP_synt_I ABC_tran ABC_tran SMC_N CbiQ UbiA PBECR4 polyprenyl_synt ? DoxD Pyr_redox_2 DHO_dh DHODB_Fe-S_bind Flavodoxin_2 Form_Nir_trans

WP_090544853.1
NZ_FOQF01000001.1:125168-140522
Pseudobutyrivibrio sp. OR37

CobD_Cbib Aminotran_1_2 Radical_SAM_C Radical_SAM IMS IMS_HHH_1 IMS_C Peptidase_S9 ? PAF-AH_p_II PBECR4 ? DUF6033 NikA-like ? LMWPc ? ?

WP_090799854.1
NZ_FNSW01000003.1:1-7987
Paenibacillus sp. GP183

? Phage_integrase PBECR4 ? DUF8426 ? ? ? MerR_1 KxDL

WP_091865782.1
NZ_FMYB01000001.1:206631-217775
Butyrivibrio sp. INlla16

CD1107-like CD1107-like Baculo_PP31 DUF4316 NikA-like MobC ? Relaxase SpoVG PBECR4 Sigma70_r2 Sigma70_r4_2 ? Receiver LytTR HATPase_c_5 FliD_C SPM Receiver LytTR

WP_118756568.1
NZ_CEVPJA010000004.1:18292-37513
Enterocloster lavalensis

PTS_EIIA_1 PTS_EIIC PTS_EIIB HTH_6 AP_endonuc_2 TOBE_2 OB_MalK ABC_tran BPD_transp_1 BPD_transp_1 SBP_bac_8 PBECR4 SpoIIE Phage_T4_gp19 Phage_sheath_1C Phage_sheath_1 DUF6861 OEP ACR_tran YknX_C BSH_RND BSH_CusB

WP_143958529.1
NZ_CP065540.1:1308380-1316178
Limosilactobacillus reuteri

? ? Phage_pRha ? ? HTH_19 Peptidase_M78 PBECR4 ? ? ? ? ? ? ?

WP_098231513.1
NZ_NTZO01000041.1:6988-12343
Bacillus sp. AFS001701

PBECR4 YdaE ? ? Acetyltransf_7 DUF4279 DUF8426 Resolvase Recombinase

WP_098839394.1
NZ_NUTA01000098.1:313-14270
Bacillus toyonensis

? Phage_integrase PBECR3 HTH_36 DUF8426 ? ? PBECR4 ? YjcZ MerR_1 ? ? ? HTH_3 ?

WP_099305912.1
NZ_FZLP01000011.1:6300-17039
Bacillus sp. Marseille-P3800

? PBECR4 DUF5986 HTH_3 Peptidase_M78 GSDH Collagen Collagen DUF2521 Amidase_3 CAT_RBD PRD PRD

WP_099314478.1
NZ_JAGZTY010000030.1:298-6982
Clostridium sp.

? PBECR4 Oxidored_q3 ? Mob_Pre RepB_primase HTH_11

WP_100733329.1
NZ_JAGSXU010000025.1:1-7750
Lactobacillus crispatus

SlpA_N SlpA_D2 SlpA SlpA PBECR4 ? ? ? HATPase_c_4 SLFN_AlbA_2 SlpA SlpA SlpA_D2 SlpA_N

WP_101877111.1
NZ_CABMKL010000001.1:2276242-2291591
Lachnoclostridium edouardi

Radical_SAM SPASM TauE ABC_tran ABC_tran ABC_ATPase CbiQ Ribosomal_L13 Ribosomal_S9 PBECR4 HD Cys_Met_Meta_PP PALP GreA_GreB_N GreA_GreB ? Acetylase ?

WP_103203176.1
NZ_CVTD020000019.1:284-6904
Herbinix hemicellulosilytica

? ? HTH_3 Receiver LytTR ? SPOB_a HATPase_c_5 PBECR4 ? TnpB_IS66 LZ_Tnp_IS66 DDE_Tnp_IS66 DDE_Tnp_IS66_C

WP_185162620.1
NZ_JACKWX010000011.1:65076-83921
Clostridium algidicarnis

Helicase_C ISP_coupler UPF0020 Type_ISP_C T1RH-like_C ? Resolvase Recombinase Zn_ribbon_recom rve_2 rve HTH_21 HTH_28 HTH_28 ? DEAD Helicase_C DbpA Lyase_1 FumaraseC_C ? WHD_CvfB S1_2 S1_2 Toprim Topoisom_bac zf_Tbcl LysM LysM Glyco_hydro_18

WP_106060509.1
NZ_PVXQ01000031.1:28177-41840
Clostridium vincentii

SseB SseB_C ? Peripla_BP_4 dCache_1 HAMP HD_5 Acetylase PBECR4 ? Flavodoxin_4 Prismane ? Hemerythrin MatE MatE Glu_cys_ligase Glu_cys_ligase ATP-grasp_6 GARS_A RimK

WP_146139950.1
NZ_PYAV01000014.1:13261-27497
Salsuginibacillus halophilus

Ribosomal_S13 Ribosomal_S11 RNA_pol_A_bac RNA_pol_A_CTD Ribosomal_L17 PseudoU_synth_1 PseudoU_synth_1 Ribosomal_L13 Ribosomal_S9 PBECR4 Chromate_transp Chromate_transp DivIVA SNIPE T5orf172 MazG-like HKD ResIII Helicase_C HNH_repeat ? Mem_trans CW_binding_2

WP_109348711.1
NZ_BJUE01000007.1:34608-45374
Kurthia zopfii

GyrI-like ? FecCD FecCD Peripla_BP_2 SIS ABC_tran SH3_3 PBECR4 ? YdeJ SH3_3 ? SH3_3 Glyco_hydro_25 Phage_holin_5_1 RNase_Y_N

WP_170090616.1
NZ_CP179918.1:2140681-2154431
Limosilactobacillus reuteri

Fic FaeA HKD Aq_aa27 Acetylase Branch_AA_trans adh_short_C2 ? PBECR4 ? DUF772 DDE_Tnp_1 ? ? DUF5388 ? Resolvase

WP_267271225.1
NZ_CP084384.1:1740899-1760817
Lactobacillus helsingborgensis

Gram_pos_anchor MucBP MucBP MucBP MucBP MucBP DUF285 ? MucBP MucBP MucBP Sortase CAT_RBD PRD PRD PTS_EIIB PTS_EIIC PTS_EIIA_1 Glyco_hydro_1 PBECR4 ABC_tran ABC_membrane FAD_binding_2 MFS_1 MFS_1 HTH_1 LysR_substrate ? PemK_toxin MazE_antitoxin

WP_265881165.1
NZ_JAJCSU010000032.1:1-11460
Clostridium perfringens

DUF4158 DDE_Tnp_Tn3 ? ? ? Phage_integrase ? ? ? ? HNH Terminase_4 TerL_ATPase TerL_nuclease Phage_portal

WP_209073524.1
NZ_CP072117.1:8648665-8665102
Cohnella sp. LGH

Aldo_ket_red Bps Receiver Trans_reg_C His-Kinase His-Kinase ABC_tran MacB_PCD FtsX FtsX VanZ PBECR4 Sigma70_r2 Sigma70_r4_2 DUF1835 ? Imm1 SMI1_KNR4 ? TerD vWA-TerF-like ?

WP_295571719.1
NZ_JBKWXH010000019.1:10320-28943
Faecalibacillus intestinalis

G5 VanW WWE TrmE_N MnmE_helical ? MS_channel_1st MS_channel_2nd MS_channel_3rd STY-kinase Meth_synt_2 ? PBECR4 DUF3427 DUF8090 Helicase_C ResIII HKD NUDIX nSTAND3 ? HNH ? ?

WP_243008641.1
NZ_QSOE01000212.1:1-3737
Anaerobutyricum hallii

? NTP_transferase VanZ ? LPD18 LPD16 PBECR4

WP_290987713.1
NZ_JAGZBP010000003.1:173628-183190
Eubacterium sp.

? AAA_14 DUF4143 ? NUDIX Peptidase_M78 Acetyltransf_7 ? PBECR4 HTH_3 Bactofilin ? Mac Hexapep ? Mac Hexapep FUR RUBY_RBDX Rubrerythrin RUBY_RBDX

WP_118264759.1
NZ_QRKY01000001.1:230798-249622
Lachnospira eligens

NUDIX ABC_membrane ABC_tran ABC_membrane ABC_tran PLDc_N HKD HKD NUDIX DegV MatE MatE PBECR4 zf-HC2 Sigma70_r4_2 Sigma70_r2 TMP-TENI HAD_2 tRNA_Me_trans tRNA_Me_trans_M tRNA_Me_trans_C Aminotran_5 Cys_Met_Meta_PP CheX Receiver

WP_270431841.1
NZ_JAQEGG010000006.1:50789-62418
Holdemanella biformis

PGA_cap SmpB Nitro_FeMo-Co tRNA_SAD tRNA-synt_2b HGTP_anticodon Phage_integrase ? DUF1828 PBECR4 ? HTH_3 ? ? SH3_5 DUF1848 TraF

WP_173900026.1
NZ_JAAILP010000018.1:394-8874
Blautia obeum

? ? HTH_26 ? BSP PIF1 SH3_13 UvrD_C_2 ? PBECR4

WP_118048264.1
NZ_QSKP01000005.1:155711-177793
Mediterraneibacter gnavus

? Acetyltransf_7 PemK_toxin DUF2513 ? ? ? PBECR4 Big ? DUF6338 DUF6558 DUF6558_C ? ? ?

WP_173702810.1
NZ_JABMHZ010000001.1:66240-86183
Blautia wexlerae

AAA_25 HTH_3 UPF0175 PDDEXK_2 ? Recombinase Resolvase FlxA Zn_ribbon_recom Recombinase Resolvase PBECR4 Glucosaminidase Amidase_2 LysM SH3_4 Phage_holin_4_1 Transposase_20 DEDD_Tnp_IS110 Lipase_GDSL ? DUF3106 Prophage_tail Prophage_tailD1

WP_119484640.1
NZ_QYJN01000002.1:239976-254540
Staphylococcus gallinarum

DUF927 ? ? Encapsidation_CP3 HTH_28 Terminase_2 ? PBECR4 ? DUF3611 Staphylokinase DUF2798 DUF2798 ? ? Lipase_2

WP_156009014.1
NZ_BCEP01000021.1:30357-44774
Streptococcus ruminantium

? ? D5_N DUF5906 Pox_D5 ? Phage_capsid Resolvase Recombinase Zn_ribbon_recom Zn_ribbon_recom PBECR4 ? WXG100 CCDC39 EsaA_helical ? ? ? ?

WP_170148477.1
NZ_RBZN01000063.1:1409-14201
Ureibacillus endophyticus

? Rep3_C Rep3_N ? TrbC Replic_Relax AAA_10 FtsK_SpoIIIE ? PBECR4 WIT1_2_N MerR_1 ? Mrr_N HTH_7 Resolvase ? ?

WP_124978509.1
NZ_BFFP01000062.1:292-6842
Ligilactobacillus salitolerans

? Phage_holin_1 Glyco_hydro_25 LysM LysM PBECR4 Acyltransferase IMS IMS_HHH_1 IMS_C

WP_125005240.1
NZ_BHYK01000035.1:118-16473
Clostridium tagluense

? TP_0214 GGDEF GAF 7TMR-DISM_7TM Hydrolase_3 dNK ? ABC2_membrane_3 Amidase_3 Rubredoxin_C Pyr_redox_2 RUBY_RBDX Flavodoxin_1 ODP DegV Sm_multidrug_ex AAA_3 AAA_lid_2 vWA ?

WP_243127739.1
NZ_RHJS01000002.1:4197289-4217145
Schaedlerella arabinosiphila

Pyr_redox_2 Fer2_BFD DAO DDE_Tnp_IS66 KIF21A_2nd DDE_Tnp_1 ? Helicase_C ResIII HKD Methyltransf_25 PBECR4 HNH_4 Y4jQ Aminotran_5 DndE AAA_23 PAPS_reduct DndB CBM_15

WP_125235971.1
NZ_RQYW01000003.1:29945-45032
Leptotrichia sp. OH3620_COT-345

CagX TrbI T4SS-DNA_transf ? T2SSE ? S1CSD-TOTE-2 PBECR4 SLT ? VirB3 VirB4_TrbE_N CagE_TrbE_VirB CagE_TrbE_VirB P-loop_TraG ? TrbL DDAH_eukar

WP_125582497.1
NZ_RHOK01000024.1:1-11919
Lacticaseibacillus suibinensis

? Phage_XkdX ? Amidase_2 PBECR4 HAMP His-Kinase His-Kinase ? ACT_4 ? ? IMS_C IMS Aldo_ket_red

WP_125605053.1
NZ_RHOX01000003.1:129265-138537
Lapidilactobacillus bayanensis

PBECR4 GLF NAD_binding_8 MurJ Polysacc_synt PS_pyruv_trans EpsG Glycos_transf_2 Glycos_transf_1 PS_pyruv_trans

WP_153453853.1
NZ_VDFL01000002.1:291180-310204
Companilactobacillus mishanensis

Acyl_transf_3 DUF1905 DUF915 PTS_EIIC AA_permease_2 GFO_IDH_MocA GFO_IDH_MocA_C3 DEAD Helicase_C PBECR4 ? ? Big Big ? PgpA DUF3290

WP_204121493.1
NZ_BOLO01000008.1:108846-130521
Levilactobacillus sp. 244-2

OB_YrrC HHH_RecD2 AAA_19 SH3_13 UvrD_C_2 Pribosyltran_N Pribosyl_synth Methyltransf_11 BPD_transp_1 SBP_bac_3 Amidase SBP_bac_5 PBECR4 GKRP_SIS_N SIS GKRP-like_C Aldo_ket_red LacI Peripla_BP_3 PfkB Transketolase_N Transket_pyr Transketolase_C_1 SH3_YKFC_2nd NLPC_P60 DUF1002

WP_127607441.1
NZ_BIMK01000050.1:1-11714
Paenibacillus chibensis

Peptidase_M24 MLTR_LBD HTH_31 ArdcN ? ? HTH_3 HTH_3 PBECR4 LMWPc Glyoxalase ? Phage_integrase 2-Hacid_dh_C DpaA_N DUF1805

WP_130783436.1
NZ_JAOPRO010000038.1:29429-41522
Bacillus paranthracis

? N_methyl ? DUF3467 Sigma70_r4 ? ? PBECR4 ? ? Acetylase Methyltransf_25 ? ? ?

WP_289649641.1
NZ_CP128470.1:1300775-1316747
Macrococcus bovicus

Prophage_tail ? Pect-lyase_RHGA_epim Beta_helix ? LRRC37AB_C Holin_SPP1 Amidase_3 LysM LysM CHAP PBECR4 NUDIX ? Trigger_N FKBP_C Trigger_C zf-C4_ClpX AAA_2 ClpB_D2-small MMR_HSR1 GlutR_N Shikimate_DH GlutR_dimer Cytochrom_C_asm

WP_136999940.1
NZ_SZNZ01000301.1:20-4228
Bacillus cereus

PBECR4 DDE_Tnp_IS240 WxL pAdhesive_11

WP_146459966.1
NZ_VOHP01000001.1:113777-132072
Streptococcus sp. sy004

Prophage_tailD1 Prophage_tail Gp58 ? ? Rav1p_C Phage_holin_1 CHAP SH3_5 PBECR4 MerR E1-E2_ATPase Hydrolase His-Kinase DNA_gyraseB Toprim DNA_gyraseB_C EzrA PUA_3 Methyltrans_SAM Com_YlbF Pyr_redox_2 Pyr_redox_dim

WP_185485233.1
NZ_JAARWK010000019.1:1-10008
Listeria innocua

? Acetylase Hol_Tox ? Fst_toxin zf-C2HCIx2C DUF3139 PBECR4 Internalin_N LRRs LRRs LRRs LRRs LRRs LRRs LRR_adjacent

WP_149172152.1
NZ_VTOY01000014.1:1633-22847
Selenomonas ruminis

HBM ? AbiEii ? Helicase_C Helicase_dom TnpV ? PBECR4 ? TrbL Peptidase_M23 ? HipA_C ? TrbL Toprim_2

WP_149475937.1
NZ_JAGGMB010000028.1:15404-24586
Oceanobacillus polygoni

? ? Zn_ribbon_Top1 PBECR4 HTH_7 Resolvase ? Glycos_transf_2 Glyco_trans_2_3 LytR_cpsA_psr LytR_cpsA_psr Gamma_PGA_hydro ? ?

WP_199690957.1
NZ_JAEHCA010000043.1:13632-25390
Bacillus cereus group sp. N24

HTH_11 Phage_integrase BPD_transp_1 BPD_transp_1 PBECR4 ? ? ? DUF3970 ? XRCC4_CC MerR_1 ALP_N

WP_154439582.1
NZ_JAHLPJ010000001.1:123626-137387
Tissierella pigra

? ? AbiEii ? ? LRRs Cu_amine_oxidN1 ? PBECR4 rve_3 rve HTH_21 HTH_Tnp_1 Nitroreductase HTH_18 AraC_binding MatE MatE TraX ?

WP_154620759.1
NZ_CBCTNG010000001.1:333369-357281
Selenomonas montiformis

Peripla_BP_1 LacI DctP DctQ DctM UxaC Mannitol_dh Mannitol_dh_C SAF GD_AH_second GD_AH_C PBECR4 TY-Chap1 Flagellin_N Flagellin_C ? POTRA_2 ShlB ? FlgM FlgN

WP_156989878.1
NZ_VWXL01000019.1:73111-84200
Caproicibacter fermentans

DnaD_N HTH_36 ? PBECR4 AgrB ? HATPase_c_5 Frag1 LytTR Receiver Lactamase_B DUF3658 DUF1835 Nmad3

WP_159641151.1
NZ_WTSV01000006.1:108931-120367
Erysipelothrix anatis

Gp53-like_C ? ? Amidase_2 CW_7 CW_7 DotZ PBECR4 ? DUF4440 AI-2E_transport Ribosom_S12_S23 Ribosomal_S7 GTP_EFTU EF-G_D2 EFG_III EFG_IV EFG_C GTP_EFTU GTP_EFTU_D2 GTP_EFTU_D3

WP_160692578.1
NZ_JAABNP010000048.1:19591-31479
Clostridium sp. C2-6-12

? Choline_bind_1 Choline_bind_2 ? Peptidase_S8 ? ? ? PBECR4 Resolvase Rod_CreS ParA-Soj-NTPase ? HTH_26 ? Choline_bind_3 Choline_bind_2

WP_306068260.1
NZ_JAROCA020000002.1:168088-184881
Tigheibacillus jepli

FUT8_N_cat Trypsin IstB_IS21 ? HTH_7 HTH_32 rve Mu-transpos_C_2 IstB_IS21 rve TnsD ? HTH_3 rve_3 rve HTH_21 HTH_Tnp_1 DUF2178 DUF4978 ? ? rve_2 rve HTH_21 HTH_Tnp_1

WP_171633492.1
NZ_WHNY01000066.1:23081-44077
Paenibacillus plantarum

His-Kinase His_kinase HAMP Peripla_BP_4 DUF2705 Receiver Trans_reg_C His-Kinase His-Kinase ABC_tran ABC2_membrane_4 PBECR4 MarR MFS_1 SLH SLH SLH Shr-like_HID GerE Receiver His-Kinase His-Kinase PAS HisKA_7TM MimR_N PAS GGDEF EAL

WP_176942308.1
NZ_JABZEC010000002.1:191506-203776
Bombilactobacillus apium

? PTS_EIIC PTS_EIIC PTS_IIA Mga ? PTS_EIIA_2 PBECR4 ? ? ThiF SPOB_a HATPase_c_5 Receiver LytTR ? LysR_substrate HTH_1

WP_320614848.1
NZ_JAXDSE010000061.1:11897-26896
Fusobacterium sp.

RNase_PH RNase_PH_C PNPase RNase_PH RNase_PH_C KH_1 S1 UPF0004 Radical_SAM TRAM_2 CDP-OH_P_transf CCB3_YggT Methyltransf_5 ? TRAM tRNA_U5-meth_tr PBECR4 Phytase-like NMT1 ABC_tran BPD_transp_1 Lactamase_B Pyr_redox_2 TetR_N

WP_288306788.1
NZ_CATXCO010000035.1:867-15007
uncultured Romboutsia sp.

AAA_15 HTH_38 Recombinase Resolvase HTH_3 Gp49 Helicase_C_2 HTH_36 PBECR4 DUF4250 ? Amidase_3 ? HTH_59 Gly_zipper HTH_7 Rab11-FIP3

WP_177975157.1
NZ_CAJMHG010000067.1:222-10936
uncultured Eubacterium sp.

FtsH_ext AAA AAA_lid_3 Peptidase_M41 Alpha-amylase_N Alpha-amylase Alpha-amylase Penicillinase_R Peptidase_M56 ? ? LytR_cpsA_psr

WP_179941327.1
NZ_JACBYF010000008.1:6973-20141
Gemelliphila palaticanis

Fe_dep_repress Fe_dep_repr_C Thymidylat_synt DHFR_1 IreB RuvX DUF1292 YceG PBECR4 zf-C4_ClpX AAA_2 ClpB_D2-small RsgA_GTPase AAA Lon_lid Lon_C MMR_HSR1 DNA_PPF LytR_cpsA_psr CpsB_CapC Wzz ParA-Soj-NTPase

WP_182528301.1
NZ_JACJHT010000027.1:5523-18962
Priestia aryabhattai

? ? FtsX_ECD MerR_1 MobA_MobL DUF3847 ? PBECR4 ? T4SS-DNA_transf ? ? ? ? ?

WP_186673893.1
NZ_JACFTD010000040.1:1-5560
Sporosarcina sp. BP05

Rep3_C Rep3_N PBECR4 ? ?

WP_187534064.1
NZ_CBCSHU010000009.1:176-8609
Erysipelothrix inopinata

PBECR4 Acetylase Peptidase_M3_N Peptidase_M3 CoA_binding_2 Flavodoxin_NdrI RNR_N Ribonuc_red_lgN Ribonuc_red_lgC Ribonuc_red_sm Thioredoxin_3

WP_191738785.1
NZ_JACSQB010000018.1:9405-26902
Clostridium faecium

? MobL ? ArdcN Peptidase_M78 Pps Pps Pps MazE_antitoxin WH_1 DUF8437 Helicase_dom Helicase_C Pps PBECR4 Pps Pps ? Leu_zip Sigma70_r4_2 Holin_BhlA ? PH_PLEKHM2 Glutaredoxin Aminotran_5

WP_191751126.1
NZ_JACSQZ010000077.1:511-11791
Clostridium gallinarum

? ? ? NikA-like PBECR4 ? TMCO5 Sigma70_r4 ? ABC_tran ? ? Cauli_VI CopG_antitoxin

WP_195337131.1
NZ_JADNDS010000018.1:73-9978
Paraclostridium bifermentans

? Zn_ribbon_CLPX_N HNH ? Resolvase ? PBECR4 Zn_ribbon_Top1 ? P97_adhes_N Phage_NinH BIG2_C

WP_201275600.1
NZ_JACVDA010000011.1:45603-62584
Parvimonas parva

Curto_V2 ? DUF3991 Toprim_2 T4SS_pilin T4SS-DNA_transf TraG-D_C DUF8208 DUF5592 TraC-like PBECR4 ? ArdcN MPTase-PolyVal ? ? ? ? ?

WP_201275875.1
NZ_JACVDA010000020.1:4817-25947
Parvimonas parva

Choline_bind_1 Choline_bind_2 Choline_bind_1 Choline_bind_2 CAP SpaA SpaA SpaA SpaA SpaA SpaA SpaA SpaA SpaA DNA_methylase Zn_ribbon_DnaG DUF3991 Toprim_2 WH_1 DUF8437 Helicase_dom Helicase_C PBECR4 ? Relaxase NikA-like DnaJ ? ? ?

WP_204653889.1
NZ_JAFBFD010000015.1:23965-36464
Enterococcus lemanii

Glyco_hydro_2 ? Peripla_BP_3 Rce1-like Cpn10 Cpn60_TCP1 CW_7 CW_7 PBECR4 DUF2568 ABC_tran FtsX SYY_C-terminal tRNA-synt_1b NAPRTase_N NAPRTase NAPRTase_C NAD_synthase ?

WP_204900928.1
NZ_JACSNZ010000019.1:24575-33634
Pseudoflavonifractor capillosus

LrgA GntR ABC_tran ? ABC_tran ? Zn_ribbon_RlmA Methyltransf_11 PBECR4 Peptidase_M3_N Peptidase_M3

WP_206813120.1
NZ_JAFLRH010000045.1:688-1296
Paradesulfitobacterium ferrireducens

PBECR4

WP_211493836.1
NZ_JADRFV010000005.1:24-15664
Fusobacterium sp. DD45

DUF4116 DUF4116 DUF4116 DUF4116 DUF4116 DUF4116 DUF4116 ? ? ? Zn_ribbon_DnaG Toprim_2 PBECR4 PBECR4 MORN_2 MORN_2 MobA_MobL NUDIX_2 MORN_2 MORN_2 MORN_2 MORN_2 MORN_2 MORN_2 MORN_2 MORN_2 MORN_2 MORN_2 MORN_2 MORN_2 MORN_2 DUF4116 DUF4116 DUF4116 DUF4116 DUF4116 DUF4116 ?

WP_213237080.1
NZ_JAHBCL010000017.1:90851-102244
Fusibacter paucivorans

CHAD DUF134 Glutaredoxin HNH_5 ADH_Fe_C Fe-ADH ? SPOUT_MTase ? STY-kinase AAA ? Glutaredoxin ? AAA_15

WP_213808360.1
NZ_JAAMFK010000001.1:56789-70253
Fructobacillus broussonetiae

GrpE HSP70 DnaJ DnaJ_C Pep_deformylase UPF0223 Inositol_P GTP_EFTU GTP_EFTU_D2 EFG_III EFG_C BipA_C PBECR4 HDC AA_permease_2 HdcB HAD_2 ? ? ?

WP_215601535.1
NZ_CP036106.1:20135-35634
Bacillus mycoides

DUF6298 ? Relaxase T4SS-DNA_transf TrbL_4 ? FKBP15 PBECR4 ? RNase_T MCPsignal CCDC39 FeeM ? Phage_integrase HTH_Crp_2

WP_215757071.1
NZ_JAHKEI010000062.1:146-652
Gemella sp. zg-1178

PBECR4

WP_216586032.1
NZ_JAHLPJ010000002.1:21194-36393
Tissierella pigra

Methylase_S Methylase_S ? N6_Mtase HsdM_N Methylase_S EcoR124_C T1R_D3-like SWI2_SNF2 REase ? ? PBECR4 YkyA Relaxase Acetylase MobC NikA-like AIPR GIY-YIG RadC ?

WP_226843914.1
NZ_JAJBMA010000012.1:11512-36653
Blautia luti

Methyltransf_11 Eco57I WH_1 DUF8437 Helicase_dom Helicase_C ArdcN YodL DUF3849 LPD18 LPD16 LPD16 TTRAP YodL LPD18 DUF4316 ? ? Sigma70_r4 RNA_pol_A_CTD PBECR4 DUF6219 Relaxase MobC NikA-like DUF6870 Resolvase Recombinase Zn_ribbon_recom DUF4368 Resolvase Recombinase Resolvase Recombinase Zn_ribbon_recom

WP_230267346.1
NZ_CAJTWK010000016.1:15320-28317
uncultured Allobaculum sp.

tRNA_bind B3_4 B5 tRNA_synthFbeta FDX-ACB GAF BPD_transp_1 Glycos_transf_2 ? SRP54_N SRP54 SRP_SPB HTH_28 PBECR4 Ribosomal_S16 KH_KhpA-B RimM PRC_RimM tRNA_m1G_MT ? Peptidase_M15_4 Ribosomal_L19

WP_239242476.1
NZ_JAKREG010000003.1:1-6962
Macrococcus epidermidis

? ? ? Terminase_4 Encapsidation_CP3 Sigma70_r4_2 ? PBECR4 DUF5067

WP_242363408.1
NZ_CAKOCC010000001.1:151402-164299
Limosilactobacillus antri

? ? HTH_59 Ion_trans ? ? ? PBECR4 ? ? Arm-DNA-bind_4 Phage_int_SAM_3 Phage_integrase LepA_C EFG_C RF3_C GTP_EFTU_D2 GTP_EFTU DnaJ_C_2 DnaJ_C DnaJ HSP70 GrpE

WP_249334750.1
NZ_JACRSY010000077.1:317-4138
Zhenhengia yiwuensis

Peptidase_C1 Cu_amine_oxidN1 Phage_holin_4_1 Amidase_2 HTH_36 PBECR2

WP_251523230.1
NZ_JAMBNS010000014.1:75503-90380
Robertmurraya korlensis

SpoIID MauE ? ABC_membrane ABC_tran MazE_antitoxin ParE-like_toxin ? PBECR4 ? ? Resolvase ? LptF_LptG Peptidase_S9 ? RamC_N STY-kinase

WP_251547925.1
NZ_CALPCI010000005.1:32136-43103
Limosilactobacillus caecicola

HTH_19 HTH_3 HTH_3 Peptidase_M78 SNIPE MUG113 Peptidase_M78 DUF5067 PBECR4 Arm-DNA-bind_4 Phage_int_SAM_3 Phage_integrase ? ? Latarcin ? IPPT DUF3042

WP_251693414.1
NZ_JAMBNV010000001.1:278000-295489
Sporosarcina luteola

EAL GGDEF PAS EamA EamA ABC_membrane ABC_tran ABC_membrane ABC_tran YusW ? DUF2804 PBECR4 Phage_integrase Phage_int_SAM_3 Sigma70_r2 Sigma70_r4_2 zf-HC2 Replic_Relax DUF7829 YolD ? Abi_C

WP_255940673.1
NZ_JANFNS010000002.1:85222-108856
Saccharibacillus sp. JS10

NHL Peptidase_M26_N SLH SLH SLH NHL Peptidase_M26_N fn3 Peptidase_M26_N Glug SLH SLH SLH ? TetR_C_8 TetR_N adh_short_C2 DUF7660 TRAM tRNA_U5-meth_tr PBECR4 ABC_tran FecCD FecCD Peripla_BP_2 Dus DEAD Helicase_C DbpA ?

WP_259138456.1
NZ_JANUXX010000005.1:98908-113135
Streptococcus sciuri

Sipho_tail Prophage_tail Collagen BppU-like_C CBM_4_9 DUF859 ? DUF7365 Phage_holin_1 Amidase_2 PBECR4 HicA_toxin HicB_lk_antitox CcdA ? ? ? HTH_3 Glyco_transf_4 Glycos_transf_1

WP_262745901.1
NZ_JAOPQX010000054.1:15556-26278
Bacillus wiedmannii

HTH_11 ? Phage_integrase MazE_antitoxin AbrB_C PBECR4 ? ? ? DUF3970 ? DAHL MerR_1 ?

WP_268938567.1
NZ_JAPTGA010000030.1:141-12726
Peribacillus sp. AS_2

? Phage_integrase TFIIE_alpha ? ? ? PBECR4 ? MerR_1 ? ?

WP_277144023.1
NZ_CP113921.1:295756-315330
Lactobacillus sp. ESL0731

Gp_dh_C Gp_dh_N HTH_1 LysR_substrate ABC_membrane ABC_tran ABC_membrane ABC_tran Peptidase_S51 DUF1706 ? PBECR4 HTH_17 ? Phosphonate-bd PTS_EIIC_2 SBP_bac_5 Gal_mutarotas_2 Glyco_hydro_31_2nd Glyco_hydro_31_3rd DUF5110 fn3 HTH_DeoR DeoRC

WP_277179885.1
NZ_CP113946.1:10184-24569
Lactobacillus sp. ESL0677

PAS_GdpP GGDEF_GdpP DHH DHHA1 Ribosomal_L9_N Ribosomal_L9_C DnaB DnaB_C Apolipoprotein Mbeg1-like MgtC UPF0236 PBECR4 ? Rce1-like TraX rve HTH_38 ? ? MerR_1

WP_277855242.1
NZ_CP120965.1:1267445-1284870
Proteiniclasticum sp. QWL-01

? ? CBM_5_12 CBM_5_12 NPV_P10 Amidase_2 SPOR Phage_holin_6_1 RepL PBECR4 DUF3800 ? MmeI_N MmeI_hel MmeI_Mtase MmeI_TRD MmeI_C ? Lipase_GDSL_2 GSDH RVT_1 GIIM

WP_302522041.1
NZ_CAUAWW010000019.1:96-10705
Parasutterella excrementihominis

LPD1 LPD5 ? ? ? PBECR4 ? TrbI CagX VirB8 MazE_antitoxin PemK_toxin ?

WP_278748043.1
NZ_JAJWLE010000123.1:1-6903
Parasutterella excrementihominis

LPD3 LPD1 LPD5 ? ? ? ? PBECR4

WP_280789102.1
NZ_JARXWM010000036.1:1-6218
Paenibacillus sp. PastF-3

HTH_24 PBECR4 ? ParB_N HTH_ParB Phage_int_SAM_2 ? ? ? ?

WP_286082705.1
NZ_CATAJS010000142.1:1-6524
Parablautia intestinalis

HNH ? ? SymE_toxin HTH_1 LysR_substrate PBECR4 PBECR4 ? ? Flavodoxin_4 Aldo_ket_red Flavodoxin_4

WP_287485576.1
NZ_JAFIKT010000010.1:3542-19540
Blautia sp.

? ? ? DEDD_Tnp_IS110 Transposase_20 PRTase-CE PCI RVT_1 PBECR4 ? ? DUF6664 HTH_3 ? Beta-lactamase MFS_2

WP_320918868.1
NZ_JAWYGK010000052.1:307-13706
Enterocloster bolteae

Ribonuc_L-PSP Collagen Collagen Collagen Collagen Collagen Collagen PBECR4 Cupin_2 HTH_3 SNF SNF LysE DUF6870 Resolvase Recombinase Zn_ribbon_recom DUF4368 BclA_C Collagen Collagen Collagen

WP_288545339.1
NZ_CAKRXB010000207.1:1-3802
uncultured Clostridium sp.

? tRNA-synt_His HisG Aminotran_1_2

WP_292212427.1
NZ_JAGBLU010000084.1:458-10169
Butyrivibrio sp.

FitA-like_RHH ? PBECR4 MCPsignal ? ECF-ribofla_trS ABC_tran DUF3744 ABC_tran CbiQ Dus ETRAMP

WP_293560098.1
NZ_JALEHY010000011.1:179-11514
Parvimonas sp.

DUF8438 DUF6796 ? PBECR4 ? Relaxase NikA-like DnaJ HTH_28 rve rve_3 HI0933_like Cytidylate_kin

WP_293959874.1
NZ_CALZLK010000045.1:1-4394
uncultured Fusobacterium sp.

? ? HK97-gp10_like Phage_tail_terminator_8 Phage_sheath_1 DUF2001 Phage_TAC_5 PBECR4

WP_294157790.1
NZ_CADBFY010000008.1:33852-44298
uncultured Selenomonas sp.

Phage_connect_1 Phage_capsid CLP_protease Gp49 HTH_3 Phage_portal ? PBECR4 TerL_nuclease TerL_ATPase DUF7678 DUF6900 DUF7698 GGACT Amidoligase_2 DUF4314

WP_294338850.1
NZ_CAKRNJ010000025.1:26836-39557
uncultured Clostridium sp.

PBECR4 HTH_7 Choline_bind_2 Choline_bind_2 Zn_Ribbon_1 ? AbiEii HTH_7

WP_294430074.1
NZ_CAMHSK010000021.1:1-19315
uncultured Treponema sp.

Receiver His-Kinase His-Kinase Y_Y_Y HD_5 ABC_tran Cu-oxidase_4 DUF5312 Phage_CI_repr SdrD_B CarboxypepD_reg Collagen DUF4959 Lcl_C PBECR4 Iso_dh ? ? sCache_3_3 HAMP HmpF MCPsignal

WP_295254056.1
NZ_JALEYZ010000048.1:32018-42252
Selenomonas sp.

HTH_3 RelE DpnD-PcfM DpnI DpnI_C N6_N4_Mtase HEPN NTP_transf_2 PBECR4 CRCB YoeB_toxin RelB DUF6339 ? ? ?

WP_296319997.1
NZ_CAMOWW010000004.1:1-11244
uncultured Treponema sp.

PfkB SpoU_methylase SpoU_sub_bind SBP_bac_8 BPD_transp_1 BPD_transp_1 HTH_18 Peripla_BP_3 Mannitol_dh Mannitol_dh_C PBECR4

WP_296328953.1
NZ_CAMNAL010000014.1:12262-31091
uncultured Treponema sp.

dCache_1 HAMP CCDC39 MCPsignal Mur_ligase Mur_ligase_M Mur_ligase_C ? Glyco_transf_28 Glyco_tran_28_C Colicin_V DNA_pol3_delta2 DNA_pol3_delta2 PDDEXK_9 AAA-ATPase_like PBECR4 Caspase Beta-prop_WDR5 Beta-prop_THOC3 KAP_NTPase DUF4384 LPP20 ? Phage_CI_repr ?

WP_296860068.1
NZ_JAFXWV010000114.1:427-7164
Treponema sp.

AIRS_C GATase_5 HTH_3 ? ? ? ? ? PBECR4

WP_296860443.1
NZ_JAFXWV010000146.1:1-8665
Treponema sp.

HTH_26 fn3 fn3 fn3 fn3 ? PBECR4 Flg_new Flg_new Flg_new LpoB Zn_ribbon_double ? HTH_3

WP_297639674.1
NZ_CAMTIG010000110.1:1-5263
uncultured Clostridium sp.

? ? MGS FAD_binding_4 BBE Se-cys_synth_N SelA GTP_EFTU

WP_298789276.1
NZ_CANLSU010000019.1:6-4591
uncultured Marinococcus sp.

DUF4145 ? Mob_Pre Cnn_1N HTH_3 HTH_3 Rep_1 PBECR4

WP_300558729.1
NZ_JASLFO010000026.1:1-3052
Companilactobacillus sp.

TetR_N Epimerase PBECR4 Cation_ATPase_C

WP_302626920.1
NZ_CALGRE010000051.1:3198-12206
uncultured Eubacterium sp.

PBECR4 PHP Calcineurin RicinB_lectin_2 CBM_6 ATP-synt_B V_ATPase_I V_ATPase_I ATP-synt_C ATP-synt_C

WP_302729248.1
NZ_JAULSA010000006.1:344878-356271
Saccharibacillus sp. CPCC 101409

Methyltransf_31 ? NUDIX AAA_18 ? MCRA Methyltransf_11 PBECR4 MCRA ? Methyltransf_25 DUF981 FAIM1 MLTR_LBD HTH_31 Epimerase

WP_303669861.1
NZ_SVCA01000008.1:144356-157352
Selenomonas ruminantium

TrkA_N TrkA_C TrkA_N TrkA_C TrkH TrkH Mem_trans Mem_trans PBECR4 Rick_17kDa_Anti ? Peripla_BP_4 ABC_tran ABC_tran BPD_transp_2 BPD_transp_2 ?

WP_303818051.1
NZ_CAMOFN010000106.1:63-6792
Selenomonas ruminantium

Glug TPS PBECR4 Glyco_hydro_77 Alpha-amylase

WP_309451869.1
NZ_JARLHR010000248.1:2670-13990
Clostridium sp.

CCDC22_CC DUF4250 RHH_1 NikA-like PBECR4 Resolvase Resolvase HTH_7 Beta-barrel_AprE HB_LcnD HB_LcnD HB_LcnD BSH_RND ABC_tran ABC_membrane Peptidase_C39 HTH_3 DUF6773 Bacteriocin_IIc

WP_311246897.1
NZ_JAUZUW010000005.1:141035-158886
Exiguobacterium sp. BRG2

GCP_N_terminal ? ? ? ? ? YolD PBECR4 Phage_int_SAM_1 Phage_integrase DUF4365 Helicase_C_2 ResIII DUF4131 Excalibur LysR_substrate HTH_1

WP_311983940.1
NZ_JARQCC010000002.1:367379-380181
Vagococcus carniphilus

DEAD Helicase_C Acetyltransf_10 Hydrolase_4 Hydrolase_4 tRNA-synt_2c tRNA_SAD DHHA1 AKAP9_coil_N CsbD Phage_integrase Phage_int_SAM_3 Arm-DNA-bind_4 PBECR4 ? Peptidase_M78 HTH_3 ? Bro-N ANT HTH_17 N6_Mtase

WP_311984578.1
NZ_JARQCC010000022.1:2641-10308
Vagococcus carniphilus

? ? Prim-Pol PriCT_1 VapE-like_dom ? ? Terminase_2 PBECR4 Resolvase

WP_314084991.1
NZ_CAUPZX010000010.1:34167-42218
uncultured Gemella sp.

Gp58 Peptidase_S74 DUF641 CBM_5_12 Sialidase ? ? Phage_holin_5_2 PBECR4 CHAP SH3_5

WP_314397002.1
NZ_CAURJN010000013.1:20152-37345
uncultured Gemella sp.

Acetate_kinase PolyA_pol PolyA_pol_RNAbd tRNA_NucTran2_2 RNase_T N-OB tRNA-synt_2 DnaD_N DnaB_2 HhH-GPD Peptidase_A8 Pox_F15 Methyltransf_1N DNA_binding_1 Formyl_trans_N Formyl_trans_C NusB RsmF-B_ferredox Methyltr_RsmB-F RlmN_N Radical_SAM PP2C_2 PP2C STY-kinase Orf78 PASTA PASTA PASTA GIY-YIG UvrC_M UVR UvrC_RNaseH Antimicrobial_7 UvrC_RNaseH_dom HHH_5

WP_314348573.1
NZ_CAUQVI010000002.1:419-8752
Granulicatella elegans

Isochorismatase PBECR4 Synaptojanin LuxS 60KD_IMP Acylphosphatase DUF1033 FtsK_alpha FtsK_SpoIIIE FtsK_gamma DUF7649 LiaF-like_C

WP_314406152.1
NZ_CAURMG010000002.1:10772-24292
uncultured Gemella sp.

NAD_binding_10 Methyltransf_31 Cupin_2 SSB DUF2087 MFS_1 MFS_1 PBECR4 Exo_endo_phos_3 FolB HPPK Dus PK PK PK_C Sortase MFS_1

WP_314548034.1
NZ_CAUSAI010000003.1:4332-21121
uncultured Gemella sp.

Acetate_kinase PolyA_pol PolyA_pol_RNAbd tRNA_NucTran2_2 RNase_T N-OB tRNA-synt_2 DnaD_N DnaB_2 HhH-GPD Peptidase_A8 PBECR4 Methyltransf_1N DNA_binding_1 Formyl_trans_N Formyl_trans_C NusB RsmF-B_ferredox Methyltr_RsmB-F RlmN_N Radical_SAM PP2C_2 STY-kinase PASTA PASTA PASTA GIY-YIG UvrC_M UVR UvrC_RNaseH Antimicrobial_7 UvrC_RNaseH_dom HHH_5

WP_314655039.1
NZ_CAUUEI010000066.1:160-11342
uncultured Selenomonas sp.

RE_endonuc ResIII N6_N4_Mtase DUF4391 Helicase_C ResIII HTH_23 Resolvase PBECR4

WP_317856075.1
NZ_CP092441.1:1307000-1324561
Chakrabartyella piscis

? HTH_Tnp_1 HTH_21 rve rve_2 DUF4315 CD1107-like CD1107-like rve_2 rve HTH_21 HTH_Tnp_1 HEPN_Cthe2314 LPD18 DUF4316 PBECR4 ? ? HTH_Tnp_1 HTH_21 rve rve_2 ? ? Fe_dep_repr_C Fe_dep_repress ABC_tran ABC_membrane

WP_317936229.1
NZ_JAUBDH010000007.1:166-12373
Sporosarcina aquimarina

? Peptidase_M3 Peptidase_M3_N Dynamitin ? Beta-lactamase2 ? Beta_helix Beta_helix Beta_helix AAA AAA_lid_6 RuvB_N AAA AAA_lid_6 Wzz GNVR CoA_binding_3 Polysacc_synt_2

WP_317989176.1
NZ_CAKXID010000044.1:1-7968
Faecalibacillus intestinalis

DUF4365 ? Lactamase_B ? Fer4_7 NTP_transferase ? ? DEDD_Tnp_IS110

WP_320314574.1
NZ_JAVIKH010000024.1:13784-21820
Candidatus Cetobacterium colombiensis

RelB ? ? Zeta_toxin ? Cas12f1-like_TNB OrfB_IS605 Y1_Tnp PBECR4 ? ? ParA-Soj-NTPase ParB_N Rep3_N

WP_320630334.1
NZ_JAXDRT010000021.1:1-15154
Parvimonas sp.

SpaA LPD11 Zn_ribbon_DnaG DUF3991 Toprim_2 TrbC T4SS-DNA_transf TraG-D_C DUF8208 DUF5592 TraC-like PBECR4 ? ResIII Lysozyme_like NLPC_P60 ArdcN MPTase-PolyVal ? ? ?

WP_321110276.1
NZ_JAXFSW010000029.1:1-4003
Agathobacter sp.

PBECR4 T4SS-DNA_transf PAP2

WP_323394305.1
NZ_JAYFOP010000067.1:1-11024
Sphaerochaeta associata

AAA_11 AAA_12 DUF2726 DDE_Tnp_IS1595 ? PBECR4 ? ? Phage_integrase Phage_int_SAM_1 ? NAD_binding_8

WP_330002720.1
NZ_JAXJEF010000016.1:1-12193
Evtepia sp.

SLH SLH YpuD_C PBECR4 ABC_sub_bind BPD_transp_2 ABC_tran Phage_int_SAM_3 Phage_integrase ? SLH

XME04322.1
CP175961.1:2011945-2026092
Lachnospiraceae bacterium C1.1

? ? ? ? Epimerase UDPG_MGDP_dh_C UDPG_MGDP_dh UDPG_MGDP_dh_N DUF4422 PBECR4 C2185-like_N Radical_SAM C2185-like_N Gly_transf_sug Glycos_transf_2 Hydrolase_like PNK3P SIS_2 CTP_transf_like PfkB Methyltransf_11 C2185-like_N